

GenCore version 5.1.6
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OK protein - nucleic search, using frame_plus_p2n model

Run on: April 22, 2004, 05:19:48 ; Search time 391 Seconds
(without alignments)
2238.181 Million cell updates/sec

Title: US-09-935-390A-23
Perfect score: 1167
Sequence: 1 MERRHPVCSGTQPTQFRCS.....TVSTTDEHLVYNHTTRPL 206

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSELOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*

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2:	Geneseqn1990s:*
3:	Geneseqn2000s:*
4:	Geneseqn2001as:*
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9:	Geneseqn2003cs:*
10:	Geneseqn2004s:*

PreC. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1167	100.0	1505	2	AAV43604 Human sec
2	1167	100.0	1542	2	AAT90038 Hepatocyt
3	1167	100.0	1542	2	AAX02200 Human HAI
4	1167	100.0	1870	3	AAL46725 Human pro
5	1163	99.7	2482	4	AAF30055 Human cDN
6	1163	99.7	2482	4	AAD16721 Human hep
7	1163	99.7	2482	6	ABK40259 cDNA enco
8	1163	99.7	2482	6	ABL88092 Human PRO

9	1163	99.7	2482	6	ABK69965	Abk69965	CDNA enco
10	1163	99.7	2482	6	ABL95581	AbL95581	Human ang
11	1163	99.7	2482	8	ADA01277	Ada01277	Human PRO
12	1163	99.7	2482	8	ADA43706	Ada43706	Human CDN
13	1163	99.7	2482	8	ADA43474	Ada43474	Human CDN
14	1163	99.7	2482	8	ADA01149	Ada01149	Human PRO
15	1163	99.7	2482	8	ADA01033	Ada01033	Human CDN
16	1163	99.7	2482	8	ADA43590	Ada43590	Human CDN
17	1163	99.7	2482	8	ADA06852	Ada06852	Human PRO
18	1163	99.7	2482	8	ADA08340	Ada08340	Novel hum
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21	1163	99.7	2482	8	ADB66071	ADB66071	Human CDN
22	1163	99.7	2482	9	ADB99749	ADB99749	Human PRO
23	1163	99.7	2482	9	ADB99404	ADB99404	Novel hum
24	1163	99.7	2482	9	ADB65955	ADB65955	Human CDN
25	1163	99.7	2482	9	ADC23353	ADC23353	Human CDN
26	1163	99.7	2482	9	ADC26046	ADC26046	Human PRO
27	1163	99.7	2482	9	ADD10330	ADD10330	Human sec
28	1163	99.7	2482	9	ADD11290	ADD11290	Human sec
29	1163	99.7	2482	9	ADD37083	ADD37083	Human sec
30	1163	99.7	2482	9	ADE04873	ADE04873	Human PRO
31	1163	99.7	2482	9	ADE11179	ADE11179	Human PRO
32	1163	99.7	2482	9	ADD88110	ADD88110	Human PRO
33	1163	99.7	2482	9	ADD95405	ADD95405	Human CDN
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37	1163	99.7	2482	9	ADD90807	ADD90807	Human CDN
38	1163	99.7	2482	10	ADE51660	ADE51660	Human CDN
39	1163	99.7	2482	10	ADE51776	ADE51776	Human CDN
40	1163	99.7	2482	10	ADE37634	ADE37634	Human CDN
41	1163	99.7	2482	10	ADE37518	ADE37518	Human CDN
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45	1163	99.7	2482	10	ADE39401	ADE39401	Human PRO

ALIGNMENTS

RESULT 1
AAV43604

ID AAV43604 standard; DNA; 1505 BP.

XX AAV43604;

XX 24-SEP-1998 (first entry)

XX Human secreted protein 4 encoding DNA.

XX Secreted protein; human; cell proliferation; cytokine activity;
XX tissue growth; cellular differentiation; regeneration; inhibin;
XX chemotactic; haemostatic; thrombolytic; tumour inhibition;
XX anti-inflammatory activity; biomarker; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 171..791

FT /tag= a

FT /product= "human secreted protein"

XX WO9825959-A2.

XX 18-JUN-1998.

XX 11-DEC-1997; 97WO-US022787.

XX 11-DEC-1996; 96US-0032757P.

XX (CHIR) CHIRON CORP.

PI Escobedo J, Hu Q, Garcia P, Williams LT, Kothakota S;

XX WPI; 1998-348453/30.
DR P-PSDB; AAW63684.

XX Secreted human polypeptides - having cytokine, cell proliferation or
PT differentiation, activin or inhibin, tumour inhibition or anti-
PT inflammatory activities.

XX Claim 6; Page 31-32; 78pp; English.

XX This DNA encodes a human secreted protein. The specification provides
CC secreted protein sequences (AAW63681 to AAW63693) encoded by the nucleic
CC acid sequences shown in AAV43601 to AAV43619. The invention provides a
CC method of identifying a secreted polypeptide which is modified by rough
CC microsomes. The secreted proteins can be used in assays to determine
CC biological activities, such as cytokine, cell proliferation, or cellular
CC differentiation activities, tissue growth or regeneration, activin or
CC inhibin activity, chemotactic or chemokinetic activity, haemostatic or
CC thrombolytic activity, receptor/ligand activity, tumour inhibition, or
CC anti-inflammatory activity. The proteins can also be used as biomarkers,
CC to identify tissues or cell types which express the proteins, or a stage-
CC or disease-specific alteration in protein expression. They can be used in
CC protein interaction assays, to identify ligands or binding proteins.
CC Compounds which affect the biological activities of the secreted proteins
CC or their ability to interact with specific ligands can be identified
CC using the proteins in screening assays. The proteins and antibodies that
CC bind specifically to the protein can also be used to design diagnostic
CC tests and therapeutic compositions for diseases which may be associated
CC with altered expression of these proteins. Fusion proteins comprising,
CC e.g. signal sequences or transmembrane domains of the proteins can be
CC used to target other protein domains to cellular membrane or they can be
CC secreted extracellularly

SQ Sequence 1505 BP; 332 A; 450 C; 406 G; 317 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7,51e-115 Length: 1505
Score: 1167.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-935-390A-23 (1-206) x AAV43604 (1-1505)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 171 ATGGAAGAGCGCCATCCAGTGTGCTCTGGCACCTGTGAGCCACCCAGTTCCTCGTGAGC 230

QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 231 AATGGCTCTGTCATCGACAGATTTCCTGGAGTGTGACGACACCCCACTGCCCGGACGCC 290

QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 291 TCCGACGAGGCTGCCTGTGAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 350

QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 351 TTCCCGACGACAAAGGGCACTGGTGACCTGCCAGACACAGGACTCTGCAAGGAGGC 410

QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 411 ATCCCGCGCTGGTACTACACCCCTTCAGCGAACAACCTGGCCCGCTTTACCTATGGTGGT 470

QY 101 CysTyrGlyAsnLysAsnAspPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db 471 TGTACGGCAACAAGAACTTTGAGGAAGACAGAGTGCCTCGAGTCTTGTGCGGCGC 530

QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db 531 ATCTCCAAGAAGGATGTGTTGGCCTGAGCGGGGAATCCCATTCACGACAGGCTCT 590

QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db 591 GTGGAGATGGCTGTCCAGTGTTCCTGGTCTCATCTGCATTGTGGTGGTAGCATCTTG 650
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 651 GGTACTGCTTCTTCAAGAACCCAGAGAAAGGACTTCCACCGGACACACCCACCA 710
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 711 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACCGAGACCTGGTCTATAAC 770
QY 201 HisThrThrArgProLeu 206
Db 771 CACACCAAGCGGCCCTC 788

RESULT 2

AAAT90038

ID AAT90038 standard; cDNA to mRNA; 1542 BP.

XX AAT90038;

AC AAT90038;

XX 21-NOV-1997 (first entry)

XX Hepatocyte growth factor activator inhibitor cDNA.

DE Inhibition; inhibitor; protease; hepatocyte; growth factor; activation;

XX activator; human; cancer; cell line; MKN45; regulation; regulator;

KW antibody; kinetic study; assay standard; ds.

XX Homo sapiens.

XX Key

PH CDS

FT 1..1542

FT /tag= a

FT sig_peptide

FT /tag= b

FT mat_peptide

FT 109..1539

FT /tag= c

FT /product= "HGFA_inhibitor"

XX EP759467-A2.

PN 26-FEB-1997.

XX 23-JUL-1996; 96EP-00111870.

XX 24-JUL-1995; 95JP-00187135.

XX (MITU) MITSUBISHI CHEM CORP.

PA Shimomura T, Kawaguchi T, Kitamura N, Miyazawa K;

XX WPI; 1997-147516/14.

XX P-PSDB; AAW27368.

XX New hepatocyte growth factor activator inhibitor and DNA - regulates

PT hepatocyte growth factor and/or HGF activator in vivo or in vitro, and

PT are used in kinetic studies.

XX Claim 10; Page 28-30; 38pp; English.

XX The present sequence encodes an inhibitor of the protease activity of

CC hepatocyte growth factor (HGF) activator (HGFA), which has a molecular

CC weight of about 40 kD when determined by SDS-PAGE. The inhibitor, which

CC was isolated from the human cancer cell line MKN45, can be used as an in

CC vivo or in vitro regulatory factor for HGF or HGFA. It can also be used

CC to raise antibodies, useful in kinetic studies of the inhibitor, or as

CC assay standards

XX Sequence 1542 BP; 319 A; 507 C; 439 G; 277 T; 0 U; 0 Other;

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Alignment Scores:
Pred. No.: 7,76e-115 Length: 1542
Score: 1167.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-935-390A-23 (1-206) x AAT90038 (1-1542)
QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db ATGGAAGGCGCCATCCAGTGTCTGCGCACCTGTCAGCCCACTGTCGGCTCGCAGC 981
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db AATGGCTGTGTCATCGACAGTTTCTGGAGTGTGACGACACCCCACTGCCCGCAGCC 1041
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db TCCGACGAGGCTGCTGTGAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1101
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db TTCCCGAGTGACAAAGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGAGAGC 1161
QY 81 IleProArgTyrTyrTyrAsnProPheSerGluHisCysAlaArgPheThrGlyGly 100
Db ATCCCGCGCTGGTACTACACCCCTTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGT 1221
QY 101 CysTyrGlyAsnLysAsnAsnAsnGluGluGluGlnCysLeuGluSerCysArgGly 120
Db TGTATGGCAACAAGAACACTTTGAGGAAGAGCAGAGTGCCTCGAGTCTTGTGCGGC 1281
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db ATCTCCAAGAGGATGTGTTGGCTGAGCGGGGAATCCCATTTCCAGCAGAGGCTCT 1341
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db GTGGAGATGGTGTGCGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1401
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro 180
Db GGTTACTGCTTCTTCAAGAACCAAGAGGACTTCCAGGACACCCACCCACCA 1461
QY 181 ProThrProAlaSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACCGAGCAGCTGGTCTATAAC 1521
QY 201 HisThrThrArgProLeu 206
Db CACACACCCCGGCCCTC 1539

RESULT 3
AAX02200
ID AAX02200 standard; DNA; 1542 BP.
XX AC AAX02200;
XX DT 30-APR-1999 (first entry)
XX DE Human HAI-1 cDNA.
XX KW Hepatocyte growth factor; HAI-1; HGF inhibiting factor; human; plasmin;
XX KW treatment; prevention; protease activity; plasma; urokinase; trypsin; ss.
XX OS Homo sapiens.
XX FH location/Qualifiers
XX FT 1..1542
XX FT /*tag= a
XX FT /product= "HAI-1"
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sig_peptide 1..105
mat_peptide /*tag= b
106..1539 /*tag= c
JP11035480-A.
XX 09-FEB-1999.
XX 15-JUL-1997; 97JP-00189480.
XX 15-JUL-1997; 97JP-00189480.
XX (MITU ) MITSUBISHI CHEM CORP.
XX WPI; 1999-186215/16.
XX P-PSDB; AAW92653.
XX A preventive and/or treating agent for the diseases caused by the
exasperation of activity of protease - inhibits protease activity of
hepatocyte growth factor (HGF) activator.
XX Claim 7; Page 6-8; 8pp; Japanese.
XX This invention describes a preventive and/or treating agent for the
diseases caused by the exasperation of activity of protease of plasma
kallikrein, plasmin, urokinase and trypsin. The agent contains a protein,
HAI-1 which has the following properties, M.W. of ca. 40,000 to 57,000
Dalton by SDS-PAGE and an activity of inhibiting protease activity of
hepatocyte growth factor (HGF) activator. The HGF inhibiting activity of
the protein is specific. HAI-1 shows a high inhibiting activity on
plasmin, trypsin, HGF activator and plasma kallikrein but substantially
no inhibiting activity on thrombin. This sequence encodes the human HAI-1
protein
XX Sequence 1542 BP; 319 A; 507 C; 439 G; 277 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.: 7,76e-115 Length: 1542
Score: 1167.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
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QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 922 ATGGAAGGCGCCATCCAGTGTCTGCGCACCTGTCAGCCCACTGTCGGCTCGCAGC 981
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db AATGGCTGTGTCATCGACAGTTTCTGGAGTGTGACGACACCCCACTGCCCGCAGCC 1041
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db TCCGACGAGGCTGCTGTGAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1101
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db TTCCCGAGTGACAAAGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGAGAGC 1161
QY 81 IleProArgTyrTyrTyrAsnProPheSerGluHisCysAlaArgPheThrGlyGly 100
Db ATCCCGCGCTGGTACTACACCCCTTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGT 1221
QY 101 CysTyrGlyAsnLysAsnAsnAsnGluGluGluGlnCysLeuGluSerCysArgGly 120
Db TGTATGGCAACAAGAACACTTTGAGGAAGAGCAGAGTGCCTCGAGTCTTGTGCGGC 1281
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
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Db 1282 ATCTCCAAGAAGGATGTGTTGGCTGAGCGGGAAATCCCATTCACAGAGGCTCT 1341
QY 141 ValGluMetAlaValAlaValPheLeuValLleCysIleValValValAlaLeu 160
Db 1342 GTGGAGATGGCTGTGCGAGTGTCTGTCATCTGTCATGTGGTGGTGGTGGTGGT 1401
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 1402 GGTACTGCTTCTTCAAGAACAGAGAAAGGACTTCCACGGACACACACCCACCA 1461
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 1462 CCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1521
QY 201 HisThrThrArgProLeu 206
Db 1522 CACACACCGGCCCTC 1539

RESULT 4

AAL46725

ID AAL46725 standard; DNA; 1870 BP.

XX AAL46725;

XX 08-AUG-2002 (first entry)

XX Human protease associated protein HPRAP-2 coding sequence.

DE Human; protease associated protein; HPRAP; cancer; inflammation;
XX anti-HIV; antianaemic; antiarteriosclerotic; antidiabetic; nephrotropic; cytostatic;
KW antiinflammatory; hepatotropic; antidiabetic; nephrotropic; antigout;
KW antithyroid; immunosuppressive; thyromimetic; virucide; dermatological;
KW neuroprotective; cardiac; osteopathic; antiarthritic; antiparasitic;
KW antipsoriatic; uropathic; ophthalmological; antirheumatic; tranquiliser;
KW vulnery; antiulcer; immune disorder; gene therapy; HPRAP-2; gene; ds.
XX Homo sapiens.

OS Key Location/Qualifiers
XX CDS 134..1180
FH /*tag= a
FT /product= "HPRAP-2"
XX

PN W09957274-A1.

XX 11-NOV-1999.

XX 28-APR-1999; 99WO-US009190.

XX 01-MAY-1998; 98US-00071709.

XX (INCY-) INCYTE PHARM INC.

XX Hillman JL, Tang YT, Lai P, Corley NC, Guegler KJ, Patterson C;

XX WPI; 2000-062147/05.

XX P-PSDB; AAO17713.

PT Novel human protease associated proteins used for, e.g. the diagnosis and
PT prevention of cell proliferative and immune disorders.
XX Claim 9; Page; 75pp; English.

XX The present invention provides the protein and coding sequences of four
CC human protease associated proteins, designated HPRAP-1, HPRAP-2, HPRAP-3
CC and HPRAP-4. Human protease associated proteins are expressed in cancer
CC and immortalised cell lines and tissues associated with inflammation and
CC the immune response, and so appear to play a role in cell proliferation
CC and immune disorders. The sequences can be used to diagnose, treat or
CC prevent cell proliferative and immune disorders, including actinic
CC keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis,
CC hepatitis, mixed connective tissue disease, myelofibrosis, paroxysmal
CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary

CC thrombocythaemia, AIDS, Addison's disease, adult respiratory distress
CC syndrome, allergies, ankylosing spondylitis, amyloidosis, anaemia,
CC asthma, atherosclerosis, autoimmune haemolytic anaemia, autoimmune
CC thyroiditis, bronchitis, cholecystitis, contact dermatitis, Crohn's
CC disease, atopic dermatitis, dermatomyositis, diabetes mellitus,
CC emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis
CC fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis,
CC Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis,
CC hyper eosinophilia, irritable bowel syndrome, multiple sclerosis,
CC myasthenia gravis, myocardial or pericardial inflammation,
CC osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
CC Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome,
CC systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis,
CC thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome,
CC infections and trauma. The present sequence is the HPRAP-2 coding
CC sequence. Note: The present sequence is not obtainable from this Derwent
CC basic but was obtained from the Derwent family equivalent US6171790
XX

SQ Sequence 1870 BP; 416 A; 558 C; 510 G; 386 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1e-114 Length: 1870
Score: 1167.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-935-390A-23 (1-206) x AAL46725 (1-1870)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 560 ATGGAAGGCGCCATCCAGTGTGCTCTGGCACCTGTGAGCCACCCAGTTCGGTGCAGC 619
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db 620 AATGGCTGCTGCATCGACAGTTTCCTGGAGTGTGACGACACCCCACTGCCCGGCGCC 679
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 680 TCCGACGAGGCTGCCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 739
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 740 TTCCCCAGTGACAAAGGCGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGC 799
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 800 ATCCCGCGCTGGTACTACAAACCCCTTCAGCGACACTGCGCCCGCTTTACTATGGTGGT 859
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db 860 TGTATGGCAACAAGAACAACTTTGAGGAGAGCAGCAGTGCTCGAGTCTTGTGCGGCGC 919
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db 920 ATCTCCAAGAAGGATGTGTTGGCTTGAGGAGAGCAGCAGTGCTCGAGTCTTGTGCGGCGC 979
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
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QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 1040 GGTACTGCTTCTTCAAGAACACAGAGAAAGGACTTCCACGGACACACACCCACCA 1099
QY 181 ProThrProAlaSerSerThrValSerThrGluAspThrThrGluHisLeuValTyrAsn 200
Db 1100 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1159
QY 201 HisThrThrArgProLeu 206
Db 1160 CACACCAACCGGCCCTC 1177

RESULT 5
 AAF30055
 ID: AAF30055 standard; cDNA; 2482 BP.
 XX
 AC AAF30055;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Human cDNA encoding PRO256.
 XX
 KW PRO256; UNQ223; human; immune disease; autoimmune disease; antirheumatic;
 XX antiarthritic; antiinflammatory; antianaemic; immunosuppressive;
 KW antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide;
 KW dermatological; antipsoriatic; antiasthmatic; antiallergic;
 KW immunostimulant; protease inhibitor; ss.
 XX
 OS Homo sapiens.
 XX
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 FT /*tag= b
 FT mat_peptide 293..1774
 FT /*tag= c
 FT
 PN WO200105972-A1.
 XX
 PD 25-JAN-2001.
 XX
 PF 15-MAR-2000; 2000WO-US006884.
 XX
 PR 20-JUL-1999; 99US-0144758P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ;
 PI Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D;
 PI Watanabe CK, Wood WI;
 XX
 DR WPI; 2001-103149/11.
 DR P-PSDB; AAB20113.
 XX
 PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for
 PT diagnosing and treating immune-related disorders, such as multiple
 PT sclerosis, rheumatoid arthritis and diabetes.
 XX
 PS Claim 21; Fig 11; 127pp; English.
 XX
 CC The present sequence is that of cDNA clone DNA35880-1160 (ATCC 209379)
 CC encoding novel human immunomodulator protein PRO256 (UNQ223) (see
 CC AAB20113). The clone was isolated from a human placenta cDNA library. The
 CC predicted protein (58 kDa, pI 6.22) shows homology to human bikunin,
 CC indicating protease inhibitor activity. The invention provides
 CC polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see
 CC AAB20108-20) including PRO256. Claimed compositions comprising these
 CC proteins or their agonists are useful for increasing infiltration of
 CC inflammatory cells into a tissue of a mammal, stimulating or enhancing an
 CC immune response in a mammal, or increasing the proliferation of T-
 CC lymphocytes in a mammal in response to an antigen. Claimed compositions
 CC comprising the PRO polypeptide or its antagonist have the opposite
 CC effect. A claimed method for treating an immune related disorder, such as
 CC a T cell disorder, involves administering the PRO polypeptide, an agonist
 CC antibody or an antagonist antibody. The disorder is selected from
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis,
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, demyelinated diseases (such as multiple sclerosis), autoimmune
 CC chronic active hepatitis, primary biliary cirrhosis, granulomatous
 CC hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative

CC colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's
 CC disease, (auto)immune-mediated skin diseases (such as bullous skin
 CC disease, erythema multiforme and pemphigus), allergic diseases (such as
 CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and
 CC urticaria), immunologic diseases of the lung and transplantation
 CC associated diseases (such as graft rejection and graft-versus-host
 CC disease) (all claimed). Claimed methods of diagnosing these disorders
 CC comprise detecting the level of expression of the PRO gene. Also claimed
 CC are a method of identifying a compound capable of inhibiting the
 CC expression or activity of the PRO polypeptide, vectors, host cells,
 CC antibodies and a method of stimulating the proliferation of T-lymphocytes
 CC using PRO256
 XX
 SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,94e-114 Length: 2482
 Score: 1163.00 Matches: 205
 Percent Similarity: 99.51% Conservative: 0
 Best Local Similarity: 99.51% Mismatches: 1
 Query Match: 99.66% Indels: 0
 DB: 4 Gaps: 0
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 DB 1157 ATGGAAGGGCGCCATCCAGTGTGCTCTGGCACCTGTGAGCCACCCAGTTCCTCGTCGAGC 1216
 QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
 DB 1217 AATGGCTGCTGCATCGACAGTTCTCTGGAGTGTGAGACACACCCCAACTGCCCGGAGGCC 1276
 QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
 DB 1277 TCCGACGAGGCTGCTGTGAAATAATACACGAGTGGCTTTCAGGAGCTCCAGCGCATCCAT 1336
 QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
 DB 1337 TTCCCGCAGTGACAAGGGCACTGGTGACCTGCCAGACACAGGACTCTGCAAGAGAGAGC 1396
 QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
 DB 1397 ATCCCGCGCTGGTACTACACACCTTTCAGCGAACACTGGCCCGCTTTTACCTATGGTGGT 1456
 QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
 DB 1457 TGTATGGCAACAAGAACACTTTCAGGAAGAGAGAGAGAGTGCCTCGAGTCTTGTGCGGC 1516
 QY 121 IleSerIlyLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
 DB 1517 ATCTCCAGAAGGATGTGTGTGGCTGAGCGGGGAATCCCATTTCCAGCACAGGCTCT 1576
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
 DB 1577 GTGGAGATGGCTGTACACAGTGTTCCTGGTTCATCTGCATTGTGGTGTGTAGCATCTTG 1636
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro 180
 DB 1637 GGTACTGCTTCTTCAAGAACACAGAGAGAGAGTTCACGAGACACCCACACACCCACCA 1696
 QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
 DB 1697 CCCACCCCTGCCAGTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1756
 QY 201 HisThrThrArgProLeu 206
 DB 1757 CACACACCCCGGCCCTC 1774
 RESULT 6
 AAD16721
 ID AAD16721 standard; cDNA; 2482 BP.
 XX

AC AAD16721;
 XX
 DT 19-NOV-2001 (first entry)
 XX
 DE Human hepatocyte growth factor activator inhibitor, PRO256 cDNA.
 XX
 KW Human; PRO256 protein; cardiovascular; endothelial; angiogenic disorder;
 KW cardiac hypertrophy; trauma; cardiac; age-related macular degeneration;
 KW gene therapy; angiogenesis; protease activity; hepatocyte growth factor;
 KW peripheral vascular disease; hepatic; renal injury; nephrotropic; tumour;
 KW restinosis; tranquillizer; vulnary; cytotatic; hepatotropic; ss.
 XX
 OS Homo sapiens.
 XX
 XX
 PH Key Location/Qualifiers
 FT CDS 188..1777
 FT /*tag= a
 FT /product= "Human hepatocyte growth factor activator
 FT inhibitor, PRO256"
 FT 188..292
 FT /*tag= b
 FT sig_peptide
 FT 293..1774
 FT /*tag= c
 FT /product= "Human mature hepatocyte growth factor
 FT activator inhibitor, PRO256"
 XX
 XX
 PN W0200159100-A2.
 XX
 PD 16-AUG-2001.
 XX
 XX 19-DEC-2000; 2000WO-US034756.
 XX
 XX 11-FEB-2000; 2000WO-US003565.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 28-NOV-2000; 2000US-0253665P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Gurney AL, Kirchhofer DK, Wood WI;
 XX
 DR WPI; 2001-541567/60.
 DR P-PSDB; AAE09332.
 XX
 PT An isolated polypeptide designated PRO256 useful for treating a
 PT cardiovascular, endothelial, or angiogenic disorder.
 XX
 PS Claim 40; Fig 1; 124pp; English.
 XX
 CC The present invention relates to PRO256 or its agonist/antagonist may be
 CC used to treat a cardiovascular, endothelial, or angiogenic disorder in a
 CC mammal, especially a human with cardiac hypertrophy, trauma, a type of
 CC tumour or age-related macular degeneration. PRO256 may be administered
 CC together with a cardiovascular, endothelial, or angiogenic agent, a
 CC chemotherapeutic agent, a growth inhibitory agent, or a cytotoxic agent.
 CC PRO256 may also be used to treat the disorders above, preferably through
 CC administration via ex vivo gene therapy. PRO256 or its agonist may be
 CC used to inhibit endothelial cell growth, angiogenesis or protease
 CC activity of a hepatocyte growth factor, whereas an antagonist of PRO256
 CC may be used to stimulate endothelial cell growth, angiogenesis or
 CC protease activity of a hepatocyte growth factor. Stimulation or
 CC inhibition of the protease activity of a hepatocyte growth factor is
 CC preferably carried out where a mammal has a cardiovascular, endothelial,
 CC or angiogenic disorder selected from peripheral vascular disease, hepatic
 CC or renal injury or a restinosis disorder. The present sequence is human
 CC hepatocyte growth factor activator inhibitor, PRO256 cDNA
 XX
 SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3.94e-114 Length: 2482
 Score: 1163.00 Matches: 205
 Percent Similarity: 99.51% Conservative: 0
 Best Local Similarity: 99.51% Mismatches: 1

Query Match: 99.56% Indels: 0
 DB: 4 Gaps: 0
 US-09-935-390A-23 (1-206) x AAD16721 (1-2482)
 QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
 Db 1157 ATGGAAAGGCGCCATCCAGTGTCTCTGGACCTGTGAGCCACCCAGTTCGGTGCAGC 1216
 QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
 Db 1217 AATGGCTGTGATCGACAGTTTCTTGGAGTGTGACGACACCCCACTGCCCGACGCC 1276
 QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
 Db 1277 TCCGACGAGGCTGCTGTGAAAATAACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336
 QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
 Db 1337 TTCCCAAGTGACAAAGGCACTGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1396
 QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
 Db 1397 ATCCCGCGCTGGTACTACAACCCCTTCAGCGAACAACCTGCGCCCGCTTACCTATGGTGGT 1456
 QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
 Db 1457 TGTATGGCAACAAGAACAACTTTGAGGAGAGAGACAGTGCCTCGAGTCTTGTGCGGGC 1516
 QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
 Db 1517 ATCTCAAGAGGATGTGTGGCTTGAGCGGGGAAATCCCATTCACAGACAGGCTCT 1576
 QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
 Db 1577 GTGGAGATGGCTGTACAGTGTCTCTGTCATCTGCATTGTGTGTGTGTAGCATCTTG 1636
 QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
 Db 1637 GGTACTGCTTCTTCAAGAACCCAGAGAGAGAGACTTCCACGAGACACCAACCAACCA 1696
 QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
 Db 1697 CCCACCCCTGCCAGTCCACTGTCTCCACTACCGAGGACACGAGGACACCTGGTCTATAAC 1756
 QY 201 HisThrThrArgProLeu 206
 Db 1757 CACACACCCCGGCCCTC 1774
 RESULT 7
 ID ABK40259 standard; cDNA; 2482 BP.
 XX
 AC ABK40259;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE cDNA encoding human PRO256 polypeptide.
 XX
 KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
 KW inflammatory disorder; immune disorder; angiogenic disorder;
 KW gene therapy; cytotatic; neuroprotective; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200153486-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 11-FEB-2000; 2000WO-US003565.
 PF
 XX 08-MAR-1999; 99WO-US005028.
 PR

PR 11-MAR-1999; 99US-0123972P.
PR 11-MAY-1999; 99US-0133459P.
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 22-JUN-1999; 99US-0140653P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149395P.
PR 31-AUG-1999; 99US-0151689P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 05-JAN-2000; 2000WO-US000219.
XX

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;

DR WPI; 2002-205567/26.
DR P-PSDB; AAU86133.

XX
PT Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.

XX
PS Claim 50; Fig 11; 302pp; English.

XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The PRO
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
CC treating benign or malignant tumors (e.g. renal, kidney, bladder,
CC breast, etc), leukemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC stromal and blastococic disorders, inflammatory, immune and angiogenic
CC disorders. The polynucleotide sequences are also useful in gene therapy.
CC ABK40254-ABK40288 encode for the human PRO polypeptides of the invention
XX

SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.94e-114 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 6 Gaps: 0

US-09-935-390A-23 (1-206) x ABK40259 (1-2482)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 1157 ATGGAAAGGCGCCATCCAGTGTGCTCTGGACCTGTCCAGCCACCCAGTTCGGCTGCAGC 1216
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspala 40
DB 1217 AATGGCTGTGTCATCGACAGATTTCCTGGAGTGTGACGACACCCCACTGCCCGACGCC 1276
QY 41 SerAspGluAlaLaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 1277 TCCGACGAGGCTGCTGTGAAATAATACAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 1337 TTCCCCAGTGACAAAGGCGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1396
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
DB 1397 ATCCCGCGCTGGTACTACAAACCCCTTCAGCGAACACTGCGCCCGCTTACCTATGTTGTT 1456

QY 101 CysTyrGlyAsnLysAsnAspPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
DB 1457 TGTATGGCAACAAGAACACTTTGAGGAAGACAGAGAGTGCCTCGAGCTTTGTGGGGC 1516
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
DB 1517 ATCTCAAGAAGGATGTGTGGCTGAGGCGGGAATCCCATTTCCAGACACAGGCTCT 1576
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160
DB 1577 GTGGAGATGGCTGTACAGTGTCTCTGTCATCTGCTGTTGGTGGTGGTAGCCATCTTG 1636
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro 180
DB 1637 GGTTACTGCTTCTTCAAGAACACAGAGAAAGGACTTCCACGGACACACACACACACCA 1696
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
DB 1697 CCCACCCCTGCCAGCTCCACTGTCTCTCCACTACCGAGGACACGAGCACCTGGTCTATAAC 1756
QY 201 HistThrThrArgProLeu 206
DB 1757 CACACCAACCGGCGCCCTC 1774

RESULT 8

ABL88092
ID ABL88092 standard; cDNA; 2482 BP.
XX
AC ABL88092;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO256 cDNA sequence SEQ ID NO:41.

XX
KW Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.

XX Homo sapiens.

XX WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220664P.

PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222695P.

PR 17-AUG-2000; 2000US-00643657.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-00664610.

PR 24-OCT-2000; 2000US-0242922P.

PR 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 22-JAN-2001; 2001US-00767609.

PR 28-FEB-2001; 2001US-00796498.

28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
09-MAR-2001; 2001US-00802706.
14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-00828366.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00866028.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001WO-US017092.
30-MAY-2001; 2001US-00870574.
30-MAY-2001; 2001WO-US017443.
01-JUN-2001; 2001WO-US017800.
(GETH) GENENTECH INC.
Baker KP, Ferrara N, Gerber H, Gerritsen MS, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
WPI; 2002-090516/12.
P-PSDB; ABB84837.
One hundred and eighty seven nucleic acids encoding PRO polypeptides,
useful in diagnosis and treatment of cardiovascular (e.g. myocardial
infarction), endothelial or angiogenic disorders in a mammal.
Claim 2; Fig 41; 565pp; English.
ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,
antiangiogenic, hypotensive, vulnary and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
proteins, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
angiogenesis (such as breast carcinoma and liver carcinoma) and wound
healing. The PRO polynucleotides have applications in molecular biology,
including use as hybridisation probes, and in chromosome and gene
mapping. ABL88259 to ABL88267 represent primers and probes used in the
exemplification of the present invention
Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3.94e-114 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 6 Gaps: 0
US-09-935-390A-23 (1-206) x ABL88092 (1-2482)
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Db 1157 ATGGAAAGCGGCCATCCAGTGTGCTCTGGCACCTGTACGCCACCCAGTTCGGCTGCAGC 1216
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 1217 AATGGCTGCTGCATCGACAGTTTCTCGAGTGTGACGACACCCCACTGCCCGGACGCC 1276
QY 41 SerAspGluAlaAlaCysGluLysTyThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 1277 TCCGACGAGGCTGCTGTGTAATAATACACGAGTGGCTTTCACGAGCTCCAGCGCATCCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1337 TTCCCGAGTGACAAAGGGCACTGGGTGGACCTGCCAGACACAGGACTCTGCAGGAGAGC 1396

QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 1397 ATCCCGCGCTGGTACTACAAACCCCTTCAGGAACACATCGCCCGCTTACCTATGGTGGT 1456
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db 1457 TGTATGCAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGGC 1516
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db 1517 ATCTCAAGAAGGATGTGTTTGGCTGAGGCGGGAATCCCAATTCACGACACAGGCTCT 1576
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db 1577 GTGGAGATGGCTGTACAGTGTCTTCTGTCATCTGCATTGTGGTGGTAGCCATCTTG 1636
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 1637 GGTTACTGCTTCTTCAAGAACACAGAGAAAGGACTTCCACGAGACACACACCCACCA 1696
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 1697 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGAGGACCTGGTCTATAAC 1756
QY 201 HistThrThrArgProLeu 206
Db 1757 CACACACCCCGGCCCTC 1774
RESULT 9
ABK69965
ID ABK69965 standard; DNA; 2482 BP.
XX
AC ABK69965;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human Pro peptide #5.
XX
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
XX genetic disorder; tumour; cancer.
OS Homo sapiens.
XX
PN WO200224888-A2.
XX
PD 28-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US027099.
XX
PR 01-SEP-2000; 2000US-0223896P.
PR 05-SEP-2000; 2000US-0230621P.
PR 22-SEP-2000; 2000US-0235147P.
PR 10-NOV-2000; 2000WO-US030873.
PR 12-JAN-2001; 2001US-0261878P.
PR 16-JAN-2001; 2001US-0261910P.
PR 16-JAN-2001; 2001US-0261939P.
PR 16-JAN-2001; 2001US-0262150P.
PR 25-JAN-2001; 2001US-0264395P.
PR 02-FEB-2001; 2001US-0266421P.
PR 09-FEB-2001; 2001US-0267623P.
PR 28-FEB-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001US-0274399P.
PR 03-APR-2001; 2001US-0280982P.
PR 04-APR-2001; 2001US-0282129P.
PR 04-APR-2001; 2001US-0282199P.
PR 09-MAY-2001; 2001US-0290589P.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.

PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JP, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR P-PSDB; ABB95443.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 1; Fig 41; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention
XX
SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.94e-114 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 6 Gaps: 0

US-09-935-390A-23 (1-206) x ABL95581 (1-2482)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 1157 ATGGAAGGGCCATCCAGTGTGCTCTGGCACCTGTGAGCCACCCAGTTCGGTGCAGC 1216
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 1217 AATGGCTGCTGCATCGACAGTTCCTGGAGTGTGAGACACCCCACTGCCCGGAGCC 1276
QY 41 SerAspGluAlaAlaCysGlnLysTyrThrSerGlyPheAspGluLeuGlnArgileHis 60
Db 1277 TCCGACGAGGCTGCTGTGAAAATAACACGAGTGGTTCGACGAGCTCCAGCGCATCCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1337 TTCCCCAGTGACAAAGGGCACTGGCTGGACCTGCCACACACAGGACTCTGCAAGGAGAGC 1396
QY 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100

Db 1397 ATCCCGCGCTGGTACTACAAACCCCTTCACGCGAACACTGCGCCCGCTTTACCTATGGTGGT 1456
QY 101 CysTyrGlyAsnLysAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsn 120
Db 1457 TGTATATGGCAACACAACTTTTGGAGGAGAGCAGCAGTCCCTCGAGTCTTGTTCGCGGC 1516
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluLeuProIleProSerThrGlySer 140
Db 1517 ATCTCAAGAAAGGATGTGTGTGGCTTGGCTGAGCGGGAATCCCATTCACGACAGGCTCT 1576
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160
Db 1577 GTGAGATGGCTGTACAGTGTTCCTGGTCACTGTGATTGTGGTGTGTAGCCATCTTG 1636
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 1637 GGTACTGCTTCTTCAAGAACCCAGAGAAAGGACTTCCACGGACACACACCCACCA 1696
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 1697 CCCACCCCTGCGCAGCTCCACTGTCTCCACTACCGAGGACACGGAGACCTGGTCTATAAC 1756
QY 201 HisThrThrArgProLeu 206
Db 1757 CACACACCCCGGCCCTC 1774
RESULT 11
ADA01277
ID ADA01277 standard; cDNA; 2482 BP.
XX
AC ADA01277;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO polynucleotide #5.
XX
KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW microvascular endothelial cell; endothelial cell tube formation;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN US2003068779-A1.
XX
PD 10-APR-2003.
XX
PF 16-SEP-2002; 2002US-00245107.
XX
PR 09-MAY-2001; 2001US-0290589P.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
(GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2003-625484/59.
DR P-PSDB; ADA01278.
XX
PT Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
PT stimulating proliferation of human microvascular endothelial cells, and
PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
PT cells.
XX
PS Claim 2; Fig 9; 307pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The

invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polynucleotide of the invention.

Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.94e-114 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 8 Gaps: 0

US-09-935-390A-23 (1-206) x ADA01277 (1-2482)

QY	1	MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer	20
Db	1157	ATGGAAGCGCCCATCCAGTGTGCTCTGSCACCTGTGACCCACCCAGTTCCGCTGCAGC	1216
QY	21	AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla	40
Db	1217	AATGGCTGCTGCATCGACAGTTTCTGAGTGTGACGACACCCCACTGCCCGACGCC	1276
QY	41	SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis	60
Db	1277	TCCGACGAGGCTGCCTGTGAAATAACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT	1336
QY	61	PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer	80
Db	1337	TTCCCCAGTGACAAAGGCGACTGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGC	1396
QY	81	IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly	100
Db	1397	ATCCCGCGCTGGTACTACACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGT	1456
QY	101	CysTyrGlyAsnLysAsnAspPheGluGluGlnGlnCysLeuGluSerCysArgGly	120
Db	1457	TGTTATGGCAACAGAACACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGCGC	1516
QY	121	IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer	140
Db	1517	ATCTCCAGAAGGATGTGTTGGCTTGAGCGGGGAAATCCCATTTCCAGCACAGGCTCT	1576
QY	141	ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu	160
Db	1577	GTGGAGATGGCTGTACAGTGTCTCTGATCATGCTGTTGTTGTTGTTGTTGTTGTTGTTG	1636
QY	161	GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro	180
Db	1637	GGTTACTGCTTCTTACAGAACCCAGAGAAAGGACTTCCACGGACACCCACCACCA	1696
QY	181	ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn	200
Db	1697	CCCAACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGACACCTGGTCTATAAC	1756
QY	201	HisThrThrArgProLeu	206

Db 1757 CACACGACCGCGCCCTC 1774

RESULT 12

ADA43706

ID ADA43706 standard; cDNA; 2482 BP.

XX ADA43706;

AC ADA43706;

XX 20-NOV-2003 (first entry)

DT 20-NOV-2003 (first entry)

XX Human cDNA encoding secreted/transmembrane polypeptide PRO256.

DE ss; gene; human; PRO; secreted protein; transmembrane protein;

XX endothelial cell tube formation; chondrocyte cell differentiation;

KW microvascular endothelial cell; tumour; lung tumour; colon tumour;

KW breast tumour; prostate tumour; rectal tumour; kidney tumour;

KW liver tumour; cytostatic; vaccine.

XX

OS Homo sapiens.

XX US2003064474-A1.

PN 03-APR-2003.

PD 16-SEP-2002; 2002US-00245859.

XX 29-AUG-2001; 2001WO-US027099.

PF 18-JUL-2002; 2002US-00197942.

PR (GETH) GENENTECH INC.

XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

PI Pong S;

XX WPI; 2003-605867/57.

DR P-PSDB; ADA43707.

XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or

PT PRO21383, useful in molecular biology, chromosome and gene mapping, in

PT generating antisense RNA and DNA, and in gene therapy.

XX Claim 2; Fig 9; 308pp; English.

PS The invention relates to an isolated secreted/transmembrane (PRO)

XX polypeptide, having at least 80% sequence identity to a sequence selected

CC from any one of the 57 amino acid sequences given in specification, or to

CC a sequence encoded by a nucleic acid molecule selected from any one of

CC the nucleic acids deposited under any of the ATCC accession numbers given

CC in specification, or a sequence having at least 80% identity to PRO

CC lacking its associated signal peptide, an extracellular domain of PRO

CC with or without its associated signal peptide. Also included are vectors,

CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding

CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by

CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,

CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and

CC an oligonucleotide probe derived from any one of the above nucleotide

CC sequences. PRO6018 polypeptide is useful for stimulating the

CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080

CC and PRO21383 polypeptides are useful for stimulating the proliferation of

CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006

CC polypeptides are useful for inhibiting the proliferation of human

CC microvascular endothelial cells. PRO polypeptides are useful for

CC detecting the presence of tumour in a mammal, including tumours of lung,

CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,

CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and

CC PRO34274 polypeptides are useful for inducing endothelial cell tube

CC formation. PRO or the antibody are useful in the preparation of a

CC medicament for treating a condition responsive to PRO polypeptide. The

CC oligonucleotide probes are useful for isolating genomic and cDNA

CC nucleotide sequences, for measuring or detecting the expression of an

CC associated gene, and as antisense probes. PRO nucleic acid is useful as a

CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence encodes a PRO protein.
XX

SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.94e-114 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 8 Gaps: 0

US-09-935-390A-23 (1-206) x ADA43706 (1-2482)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 1157 ATGGAAGCGGCCAFCACAGTGTGCTCTGGCACCTGTGAGCCACCCAGTTCCGCTGCAGC 1216
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
DB 1217 AATGGCTGCTGCATCGACAGTTTCTGGAGTGTGAGACACCCCACTGCCCGGACGCC 1276
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 1277 TCCGACGAGGCTGCCTGTGAAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 1337 TTCCCGAGTGACAAAGGCACTGCGTGGACCTGCGACACAGGACTCTGCAAGGAGGC 1396
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
DB 1397 ATCCCGCGCTGTACTACAAACCCCTTCAGCGAACAACCTGCGCCCGCTTACCTATGGTGGT 1456
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
DB 1457 TGTATGGCAACAACAACAACACTTTGAGGAAGAGCAGCAGTGCTCGAGTCTTGTGCGGGC 1516
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
DB 1517 ATCTCCAGAAAGATGTGTTGGCTGAGSGGGGAATCCCAATTCAGACACAGGCTCT 1576
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
DB 1577 GTGAGATGGCTGTACAGTGTCTCTGTCATCTGCATTTGTGGTGTGGTAGCCATCTTG 1636
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
DB 1637 GGTACTGCTTCTTCAAGAACCAAGAGAAAGGACTTCCACGGACACCAACCCACCA 1696
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
DB 1697 CCCACCCCTGCCAGCTCCACTGTCTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1756
QY 201 HisThrThrArgProLeu 206
DB 1757 CACACCAACCGGCCCTC 1774

RESULT 13

ID ADA43474

XX ADA43474 standard; cDNA; 2482 BP.

AC ADA43474;

XX 20-NOV-2003 (first entry)

DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.

XX ss; gene; human; PRO; secreted protein; transmembrane protein;

KW endothelial cell tube formation; chondrocyte cell differentiation;

KW

microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.

XX Homo sapiens.

OS

XX US2003073196-A1.

PN 17-APR-2003.

XX

PD 18-SEP-2002; 2002US-00246210.

XX

PF 04-APR-2001; 2001US-0282199P.

XX

PR 29-AUG-2001; 2001WO-US027099.

PR

PR 18-JUL-2002; 2002US-00197942.

XX

PA (GETH) GENENTECH INC.

XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC;

PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

PI Fong S;

XX WPI; 2003-743814/70.

DR P-PSDB; ADA43475.

XX

PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or

PT PRO21383 useful for stimulating the proliferation or differentiation of

PT chondrocyte cells and detecting the presence of a tumor in a mammal.

XX Claim 2; Fig 9; 307pp; English.

PS The invention relates to an isolated secreted/transmembrane (PRO)

XX polypeptide, having at least 80% sequence identity to a sequence selected

CC from any one of the 57 amino acid sequences given in specification, or to

CC a sequence encoded by a nucleic acid molecule selected from any one of

CC the nucleic acids deposited under any of the ATCC accession numbers given

CC in specification, or a sequence having at least 80% identity to PRO

CC lacking its associated signal peptide, an extracellular domain of PRO

CC with or without its associated signal peptide. Also included are vectors,

CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding

CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by

CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,

CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and

CC an oligonucleotide probe derived from any one of the above nucleotide

CC sequences. PRO6018 polypeptide is useful for stimulating the

CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080

CC and PRO21383 polypeptides are useful for stimulating the proliferation of

CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006

CC polypeptides are useful for inhibiting the proliferation of human

CC microvascular endothelial cells. PRO polypeptides are useful for

CC detecting the presence of tumour in a mammal, including tumours of lung,

CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,

CC PRO189, PRO4499, PRO6308, PRO10275, PRO21207, PRO20933 and

CC PRO34274 polypeptides are useful for inducing endothelial cell tube

CC formation. PRO or the antibody are useful in the preparation of a

CC medicament for treating a condition responsive to PRO polypeptide. The

CC oligonucleotide probes are useful for isolating genomic and cDNA

CC nucleotide sequences, for measuring or detecting the expression of an

CC associated gene, and as antisense probes. PRO nucleic acid is useful as a

CC hybridisation probe, in chromosome and gene mapping, in the generation of

CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and

CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The

CC present sequence encodes a PRO protein.

XX

SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.94e-114 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 8 Gaps: 0

US-09-935-390A-23 (1-206) x ADA43474 (1-2482)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 1157 ATGGAAAGGCGCCATCCAGTGTCTCTGGCACTGTCCAGCCACCCAGTTCGGTGCAGC 1216
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db 1217 AATGGCTGTGTCATCGACAGTTTCTGTGGAGTGTGACGACACCCCACTGCCCGAGCC 1276
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 1277 TCCGACGAGGCTGCTGTGAAATAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1337 TTCCCCAGTGACAAAGGCGCACTGCTGGTGGTGTGACGACACAGGACTCTGCAAGGAGAC 1396
QY 81 IleProArgTyrTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 1397 ATCCCGCGTGGTACTACACCCCTTCCAGGAAACACTGGCCCGCTTTACCTATGGTGT 1456
QY 101 CysTyrGlyAsnLysAsnAspPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db 1457 TGTATGGCAACAAGAACAACTTTGAGGAGAGCAGCAGTCCCTCGAGTCTTGTGCGGC 1516
QY 121 IleSerLysLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer 140
Db 1517 ATCTCCAGAGGATGTGTGCTGCTGAGCGGGAATCCCACTCCAGCACAGGCTCT 1576
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db 1577 GTGGAGATGGCTGTACAGTGTCTCTGCTCATCTGCATTGTGGTGTGTAGCCATCTTG 1636
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 1637 GGTACTGCTTCTCAAGAACACAGAGAAAGGACTTCCACGGACACCAACCAACCA 1696
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 1697 CCCACCCCTGCGAGCTCCACTGTCTCCACTACCGAGGACACCGAGCACCTGGTCTATAAC 1756
QY 201 HisThrThrArgProLeu 206
Db 1757 CACACCAACCCGCGCCCTC 1774

RESULT 14

ADA01149
ID ADA01149 standard; cDNA; 2482 BP.

XX AC ADA01149;

XX XX
DT 06-NOV-2003 (first entry)

XX XX Human PRO polynucleotide #5.

XX KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW cancer; lung; colon; breast; prostate; rectum; kidney; liver;
KW microvascular endothelial cell; endothelial cell tube formation.

XX OS Homo sapiens.

XX PN US2003068782-A1.

XX PD 10-APR-2003.

XX XX 16-SEP-2002; 2002US-00245851.

XX PF 27-APR-1999; 99US-0131271P.

XX XX 29-OCT-1999; 99US-0162506P.

PR 02-DEC-1999; 99WO-US028551.

29-AUG-2001; 2001WO-US027099.
18-JUL-2002; 2002US-00197942.

XX (GETH) GENENTECH INC.

XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;

XX WPI; 2003-625487/59.
DR P-PSDB; ADA01150.

XX Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.

XX Claim 2; Fig 9; 308pp; English.

XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, rectal, kidney and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in
CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such
CC as tumours, for stimulating and inhibiting proliferation of human
CC microvascular endothelial cells and for inducing endothelial cell tube
CC formation. This sequence represents a human PRO polynucleotide of the
XX invention.

SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.94e-114 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 8 Gaps: 0

US-09-935-390A-23 (1-206) x ADA01149 (1-2482)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20

Db 1157 ATGGAAAGGCGCCATCCAGTGTCTCTGGCACTGTCCAGCCACCCAGTTCGGTGCAGC 1216

QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40

Db 1217 AATGGCTGTGTCATCGACAGTTTCTGTGGAGTGTGACGACACCCCACTGCCCGAGCC 1276

QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60

Db 1277 TCCGACGAGGCTGCTGTGAAATAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336

QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80

Db 1337 TTCCCCAGTGACAAAGGCGCACTGCTGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAC 1396

QY 81 IleProArgTyrTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100

Db 1397 ATCCCGCGTGGTACTACACCCCTTCCAGCGAACAACACTGGCCCGCTTTACCTATGGTGT 1456

QY 101 CysTyrGlyAsnLysAsnAspPheGluGluGlnGlnCysLeuGluSerCysArgGly 120

Qy 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
 Db 1697 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1756

Qy 201 HisThrThrArgProLeu 206
 Db 1757 CACACCAACCCGGCCCTC 1774

Search completed: April 22, 2004, 08:29:56
 Job time : 401 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 22, 2004, 07:00:24 ; Search time 3729 Seconds
(without alignments)
2394.386 Million cell updates/sec

Title: US-09-935-390A-23
Perfect score: 1167
Sequence: 1 MERRHPVCSGTQPTQRCSS.....TVSTTDEHLVYNHTTRPL 206

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0935390@cgn_1_1_3731 @runat_20042004_144849_10383 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_htg:*
3: gb_in:*
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16: em_fun:*
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37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1167	100.0	1505	6	BD063229	BD063229 Secreted
2	1167	100.0	1542	6	AR148260	AR148260 Sequence
3	1167	100.0	1542	6	E12898	E12898 Human cDNA
4	1167	100.0	1542	6	E21838	E21838 Preventive
5	1167	100.0	1542	6	AR237449	AR237449 Sequence
6	1167	100.0	1542	9	BT007425	BT007425 Homo sapi
7	1167	100.0	1542	12	BT009882	BT009882 Synthetic
8	1167	100.0	1870	6	AR123705	AR123705 Sequence
9	1167	100.0	1870	6	BD205506	BD205506 Human pro
10	1167	100.0	2297	9	BC004140	BC004140 Homo sapi
11	1167	100.0	2399	9	AB000095	AB000095 Homo sapi
12	1167	100.0	2486	9	BC018702	BC018702 Homo sapi
13	1163	99.7	2370	9	AY296715	AY296715 Homo sapi
14	1163	99.7	2482	6	AX077023	AX077023 Sequence
15	1163	99.7	2482	6	AX201332	AX201332 Sequence
16	1163	99.7	2482	6	AX211596	AX211596 Sequence
17	1163	99.7	2482	6	AX454456	AX454456 Sequence
18	1163	99.7	2482	6	AX490934	AX490934 Sequence
19	1163	99.7	2482	6	AX574482	AX574482 Sequence
20	1163	99.7	2482	9	AY358969	AY358969 Homo sapi
21	999	85.6	2173	10	BC005769	BC005769 Mus muscu
22	999	85.6	2534	10	BC053341	BC053341 Mus muscu
23	989	84.7	2228	10	AF099018	AF099018 Mus muscu
24	692.5	59.3	115793	9	AC025166	AC025166 Homo sapi
25	692.5	59.3	178248	9	AC012476	AC012476 Homo sapi
26	647	55.4	816	6	BD241927	BD241927 Compounds
27	647	55.4	816	6	AR237110	AR237110 Sequence
28	647	55.4	816	6	AR260603	AR260603 Sequence
29	647	55.4	816	6	AR278134	AR278134 Sequence
30	647	55.4	816	6	AR366830	AR366830 Sequence
31	647	55.4	816	6	AR370726	AR370726 Sequence
32	647	55.4	816	6	AR392231	AR392231 Sequence
33	647	55.4	816	6	AR399866	AR399866 Sequence
34	647	55.4	816	6	AR405133	AR405133 Sequence
35	647	55.4	816	6	AX106233	AX106233 Sequence
36	647	55.4	816	6	AX140524	AX140524 Sequence
37	647	55.4	816	6	AX200384	AX200384 Sequence
38	647	55.4	816	6	AX267040	AX267040 Sequence
39	647	55.4	816	6	BD070163	BD070163 Compounds
40	584	50.0	1037	6	AX067320	AX067320 Sequence
41	572	49.0	760	6	BD241950	BD241950 Compounds
42	572	49.0	760	6	AR237133	AR237133 Sequence
43	572	49.0	760	6	AR260626	AR260626 Sequence
44	572	49.0	760	6	AR278157	AR278157 Sequence
45	572	49.0	760	6	AR366853	AR366853 Sequence

ALIGNMENTS

RESULT 1

US-09-935-390A-23 (1-206) x ED063229 (1-1505)

QY	1	MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer	20
DB	171	ATGGAAGGGCCATCCAGTGTGCTCTGGCACCTGTGAGCCACCCAGTTCGGCTGCAGC	230
QY	21	AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla	40
DB	231	AATGGCTGCTGCATCGACAGATTTCCTGGAGTGTGACGACACCCCAACTGCCCGACGCC	290
QY	41	SerAspGlnAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis	60
DB	291	TCCGACGAGGTGCCCTGTGAAAAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT	350
QY	61	PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer	80
DB	351	TTCCCCAGCGACAAAGGGCACTGCGTGGACCTGCCAGACACAGACTCTGCAAGGAGAGC	410
QY	81	IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly	100
DB	411	ATCCCGCGCTGGTACTACAACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGCTGGT	470
QY	101	CysTyrGlyAsnLysAsnAsnPheGluGluGluGlnCysIleuGluSerCysArgGly	120
DB	471	TGTTACGGCAACAAGAACAACTTTGAGGARGAGCAGCAGTGCCTTCGAGTCTTGTCGGCGC	530
QY	121	IleSerLysLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer	140
DB	531	ATCTCCAAGAGGATGTGTTTGGCCTGAGCGCGGAAATCCCAATCCCAGCACAGGCTCT	590
QY	141	ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu	160
DB	591	GTGGAGATGGCTGTGCGCAGTGTTCTTGTCATCTGCATGTGGTGGTAGCATCTTG	650

FT sig peptide 1..105
FT mat peptide 106..1542.
Location/Qualifiers
source 1..1542
/organism="Homo sapiens"
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ORIGIN

Alignment Scores:
Pred. No.: 4.72e-117 Length: 1542
Score: 1167.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-935-390A-23 (1-206) x E21838 (1-1542)

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922 ATGGAAGGGGCCATCCAGTGTGCTTGGACCTGTGACCCACCCAGTTCGGTGCAGC 981
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
982 AATGGCTGCTGCATCGACAGTTTCTGGAGTGTGACGACACCCCAACTGCCCGACGCC 1041
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
1042 TCCGACGAGCTGCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1101
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
1102 TTCCCCAGTGACAAAGGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1161
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
1162 ATCCCGCGTGGTACTACAACCCCTTCAGCGAACACTGCGCGCGCTTTACCTATGGTGGT 1221
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
1222 TGTTATGGCAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGCGC 1281
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
1282 ATCTCCAAGAAGGATGTGTTGGCTGAGCGGGAATATCCCAATTCACGACACAGGCTCT 1341
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
1342 GTGGAGATGGCTGTCGAGTGTTCCTGGTGCATCTGCATTGTGGTGGTAGCCATCTTG 1401
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
1402 GGTACTGCTTCTTCAAGAACCCAGAGAAAGGACTTCCACGGACACCCACCCACCA 1461
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
1462 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1521
QY 201 HisThrThrArgProIleu 206
DB 1522 CACACACCCCGGCCCTC 1539

RESULT 5

AR237449
LOCUS AR237449 1542 bp mRNA linear PAT 20-DEC-2002
DEFINITION Sequence 8 from patent US 6465622.
ACCESSION AR237449
VERSION AR237449.1 GI:27282185
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1542)
AUTHORS Shimomura,T., Kawaguchi,T., Kitamura,N. and Miyazawa,X.
TITLE Protein, DNA coding for same and method of producing the protein
JOURNAL Patent: US 6465622-A 8 15-OCT-2002;
FEATURES Location/Qualifiers
source 1..1542
/organism="unknown"
/mol_type="mRNA"

ORIGIN

Alignment Scores:
Pred. No.: 4.72e-117 Length: 1542
Score: 1167.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-935-390A-23 (1-206) x AR237449 (1-1542)

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QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
982 AATGGCTGCTGCATCGACAGTTTCTGGAGTGTGACGACACCCCAACTGCCCGACGCC 1041
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
1042 TCCGACGAGCTGCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1101
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
1102 TTCCCCAGTGACAAAGGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1161
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
1162 ATCCCGCGTGGTACTACAACCCCTTCAGCGAACACTGCGCGCGCTTTACCTATGGTGGT 1221
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
1222 TGTTATGGCAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGCGC 1281
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
1282 ATCTCCAAGAAGGATGTGTTGGCTGAGCGGGAATATCCCAATTCACGACACAGGCTCT 1341
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
1342 GTGGAGATGGCTGTCGAGTGTTCCTGGTGCATCTGCATTGTGGTGGTAGCCATCTTG 1401
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
1402 GGTACTGCTTCTTCAAGAACCCAGAGAAAGGACTTCCACGGACACCCACCCACCA 1461
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
1462 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1521
QY 201 HisThrThrArgProIleu 206
DB 1522 CACACACCCCGGCCCTC 1539

RESULT 6

BT007425
LOCUS BT007425 1542 bp mRNA linear PRI 13-MAY-2003
DEFINITION Homo sapiens serine protease inhibitor, Kunitz type 1 mRNA,
complete cds.
ACCESSION BT007425
VERSION BT007425.1 GI:30583688
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1542)
AUTHORS Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.

TITLE Cloning of human full-length CDSs in BD Creator(TM) System Donor
vector

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1542)
AUTHORS Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.

TITLE Direct Submission

JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA

COMMENT This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the SalI and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after SalI site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
Clone distribution: <http://bioinfo.clontech.com/orfclones>.

FEATURES
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ORIGIN

Alignment Scores:
Pred. No.: 4.72e-117 Length: 1542
Score: 1167.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-935-390A-23 (1-206) x BT007425 (1-1542)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
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QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnGlnPheArgCysAla 40
Db 982 AATGGCTGCTGCAATGACAGTTTCTCGAGTGTGACGACACCCCACTGCCCGACGCC 1041

QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60

Db 1042 TCCGACGAGCGCTGCTGTGAATAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1101

QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80

Db 1102 TTCCCGAGTACAAAGGCACTGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1161

QY 81 IleProArgTrpTyrAsnProPheSerGluHisCysAlaArgPheThrThrGlyGly 100

Db 1162 ATCCCGCGCTGTACTACACCCCTTCAGCGAACACTGGCGCGCTTTACCTATGGTGGT 1221

QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnCysLeuGluSerCysArgGly 120

Db 1222 TGTATGCAACAAGAACAACTTTGAGGAGAGCAGTGGCTCGAGTCTTGTGCGCGC 1281

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Db 1522 CACACCCACCGCGCCCTC 1539

RESULT 7
BT009882
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

BT009882 1542 bp mRNA linear SYN 02-AUG-2003
Synthetic construct Homo sapiens serine protease inhibitor, Kunitz
type 1 mRNA, partial cds.
BT009882
BT009882.1 GI:32880106
FLI CDNA.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 1542)
Kalinine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Direct Submission
Submitted (17-JUL-2003) BD Biosciences Clontech, 1020 East Meadow
circle, Palo Alto, California 94303, USA
2 (bases 1 to 1542)
Kalinine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Direct Submission
Submitted (02-AUG-2003) BD Biosciences Clontech, 1020 East Meadow
circle, Palo Alto, California 94303, USA
This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the SalI and HindIII sites of the
pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after
SalI site and before 'ATG' to provide Kozak consensus sequence;
'GG' after last codon and before HindIII site to maintain reading
frame. Clone distribution: <http://bioinfo.clontech.com/orfclones>.
Location/Qualifiers
1..1542
/organism="synthetic construct"


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ORIGIN

Alignment Scores:
Pred. No.: 4.72e-117 Length: 1542
Score: 1167.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-935-390A-23 (1-206) x BT009882 (1-1542)

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QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 922 ATGGAAGGCGCCATCCAGTGTCTCTGGCACCTGTCCAGCCACCCAGTCCGCTGCAGC 981
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db 982 AATGGCTGCTGCATCGACAGTTTCTTGGAGTGACGACACCCCACTGCCCGAGCC 1041
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 1042 TCCGACGAGGCTGCTGTGAAATAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1101
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
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Db 1402 GGTACTGCTTCTTCAAGAACCCAGAGAAAGGACTTCCACGGACACACCACCCACCA 1461
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QY 201 HistThrThrArgProLeu 206
Db 1522 CACACCACCGCGCCCTC 1539
RESULT 8
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LOCUS Sequence 6 from patent US 6171790.
ACCESSION ARI23705
VERSION ARI23705.1 GI:14109066
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1870)
AUTHORS Hillman,J.L., Tang,Y.Tom., Lal,P., Corley,N.C., Guegler,K.J. and
Patterson,C.
TITLE Human protease associated proteins
JOURNAL Patent: US 6171790-A 6 09-JAN-2001;
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KEYWORDS JP 2002513572-A/2.
SOURCE Homo sapiens (human)
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REFERENCE 1 (bases 1 to 1870)
AUTHORS Hillman,J.L., Tang,T.Y., Lal,P., Corley,N.C., Guegler,K.J. and Patterson,C.
TITLE Human protease associated proteins
JOURNAL Patent: JP 2002513572-A 2 14-MAY-2002;
INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002513572-A/2
PD 14-MAY-2002
PF 28-APR-1999 JP 2000547229
PR 01-MAY-1998 US 09/071709
PI JENNIFER L HILLMAN,TOM Y TANG,PREETI LAL,NEIL C CORLEY,KARL J
PI GUEGLER,
PI CHANDRA PATTERSON
PC C12N15/09,A61K38/00,A61K45/00,A61P19/02,A61P35/00,A61P37/02,
PC C07K14/81,
PC C07K16/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02 PC
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LOCUS
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ACCESSION BC004140
VERSION BC004140.1 GI:13278722
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2297)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,K., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 2297)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590.

REMARK
COMMENT
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadansystemsbiology.org
Anup Madan, Jessica Fahey, Brin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 2 Row: a Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504328.

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ORIGIN

Alignment Scores:

Pred. No.: 7.57e-117 Length: 2297
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Query Match: 100.00% Indels: 0
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LOCUS

DEFINITION

AB000095

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

2399 bp mRNA linear PRI 04-MAR-1998
Homo sapiens mRNA for hepatocyte growth factor activator inhibitor, complete cds.

AB000095
GI:2924600
hepatocyte growth factor activator inhibitor.

Homo sapiens (human)

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (sites)

Shimomura, T., Denda, K., Kitamura, A., Kawaguchi, T., Kito, M.,

Kondo, J., Kagaya, S., Qin, L., Takata, H., Miyazawa, K. and Kitamura, N.

Hepatocyte growth factor activator inhibitor, a novel Kunitz-type

serine protease inhibitor

J. Biol. Chem. 272 (10), 6370-6376 (1997)

97197808

9045658

2 (bases 1 to 2399)

Denda, K.

Direct Submission

Submitted (24-DEC-1996)

Kimitoshi Denda, Tokyo Institute of

Technology, Department of Life Science, 4259 Nagatsuta, Midori-ku,

Yokohama, Kanagawa 227, Japan (E-mail: kdenda@bio.titech.ac.jp,

Tel: 45-924-5702, Fax: 45-924-5771)

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ACCESSION	BC018702		
VERSION	BC018702.1 GI:17511685		
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REFERENCE	1 (bases 1 to 2486)		
AUTHORS	Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
MEDLINE	22388257		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 2486)		
AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgaps-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ruben Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.		
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ORIGIN
Alignment Scores:
Pred. No.:      8.32e-117      Length:      2486
Score:          1167.00       Matches:     206
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:     100.00%      Indels:      0
DB:              9           Gaps:        0

US-09-935-390A-23 (1-206) x BC018702 (1-2486)

Qy      1  MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
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Qy      21  AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
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Qy      41  SerAspGluAlaAlaCysGluLysTyThrSerGlyPheAspGluLeuGlnArgIleHis 60
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Qy      61  PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
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Qy      141  ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
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Qy      161  GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
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Qy      181  ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyAsn 200
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Qy      201  HisThrThrArgProLeu 206
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RESULT 13
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LOCUS
DEFINITION Homo sapiens hepatocyte growth factor activator inhibitor 1B (HAI1)
mRNA, complete cds.
2370 bp mRNA linear PRI 01-JUN-2003
ACCESSION AY296715 GI:31323050
VERSION AY296715.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2370)
AUTHORS Kirchhofer,D., Peek,M., Li,W., Stamos,J., Eigenbrot,C.,
Kadthodayan,S., Elliott,J.M., Corpuz,R.T., Lazarus,R.A. and Moran,P.
TITLE Tissue-expression, protease-specificity and Kunitz domain functions
of HAI-1B, a new splice variant of hepatocyte growth factor
activator inhibitor-1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2370)
AUTHORS Yuan,J. and Moran,P.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-2003) Physiology, Genentech Inc, One DNA Way,
South San Francisco, CA 94080, USA
FEATURES
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Alignment Scores:
Pred. No.:      2.14e-116      Length:      2370
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Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 9 Gaps: 0

US-09-935-390A-23 (1-206) x AY296715 (1-2370)

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QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
DB 1117 AATGGCTGCTGCATCGACAGTTTCTGGAGTGTGACGACACCCCACTGCCCGGAGGCC 1176
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 1177 TCCGACGAGGCTGCCTGTGAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1236
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 1237 TTCCCGAGTGACAAAGGCGACTGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1296
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DB 1657 CACACCCCGGCCCCCTC 1674

RESULT 14
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DEFINITION Sequence 11 from Patent WO0105972.
ACCESSION AX077023
VERSION AX077023.1 GI:13121657
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Fong,S., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Mark,M.R., Marsters,S.A., Pitti,R.M., Tumas,D., Watanabe,C.K. and Wood,W.I.
TITLE Compositions and methods for the treatment of immune related diseases
JOURNAL Patent: WO 0105972-A 11 25-JAN-2001;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
source 1..2482

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ORIGIN

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Pred. No.: 2,26e-116 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 5 Gaps: 0

US-09-935-390A-23 (1-206) x AX077023 (1-2482)

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QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
DB 1217 AATGGCTGCTGCATCGACAGTTTCTGGAGTGTGACGACACCCCACTGCCCGGAGGCC 1276
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 1277 TCCGACGAGGCTGCCTGTGAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
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QY 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
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QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
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DB 1637 GGTTACTGCTTCTTCAAGAACCCAGAGAAAGGACTTCCACGGACACACCACCCACCA 1696
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
DB 1697 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACCGAGCACCTGTGTCTATAAC 1756
QY 201 HisThrThrArgProLeu 206
DB 1757 CACACCCCGGCCCCCTC 1774

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DEFINITION Sequence 11 from Patent WO0153486.
ACCESSION AX201332
VERSION AX201332.1 GI:15391158
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,

Stone,D.M., Watanabe,C.K. and Wood,W.i.
Compositions and methods for the treatment of tumour
Patent: WO 0153486-A 11 26-JUL-2001;
Genentech, Inc. (US)

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ORIGIN

Alignment Scores:
Pred. No.: 2.26e-116 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
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US-09-935-390A-23 (1-206) x AX201332 (1-2482)

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Db	1217	AATGGCTGCTGCATCGACAGTTTCCTGGAGTGTGACACACCCCACTGCCCGACGCC	1276
Qy	41	SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis	60
Db	1277	TCCGACGAGGCTGCCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT	1336
Qy	61	PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer	80
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Db	1397	ATCCGGCGCTGGTACTACACCCCTTCAGGAAACACTGGCCCGCTTTACCTATGGTGGT	1456
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Db	1517	ATCTCCAAGAGGATGTGTTGGCCTGAGCGGGGAATCCCATTTCCAGCACAGGCTCT	1576
Qy	141	ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu	160
Db	1577	GUGGAGATGGCTGTACAGTGTCTGTCATCTGCATTGTGGTGTGGTAGCCATCTTG	1636
Qy	161	GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro	180
Db	1637	GGTTACTGCTTCTTCAAGAACACAGAGAAAGGACTTCCACGGACACCAACCACCCACCA	1696
Qy	181	ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn	200
Db	1697	CCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGICTATAAC	1756
Qy	201	HisThrThrArgProLeu	206
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Search completed: April 22, 2004, 09:32:11
Job time : 3737 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 10:14:05 ; Search time 65 Seconds
(without alignments)
999.950 Million cell updates/sec

Title: US-09-935-390A-23
Perfect score: 206
Sequence: 1 MERRHPVCSGTCQPTQFRCS.....TVSTTDETHLVNHTTRPL 206

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	40	19.4	507	11 Q99J04	Q99J04 mus musculus
4	9	4.4	390	10 Q7XR48	Q7XR48 oryza sativ
5	8	3.9	250	10 Q8H2V9	Q8H2V9 oryza sativ
6	8	3.9	350	4 Q9NV85	Q9NV85 homo sapien
7	8	3.9	350	4 Q9H813	Q9H813 homo sapien
8	8	3.9	350	11 Q9CZV9	Q9CZV9 mus musculus
9	8	3.9	350	11 Q9D771	Q9D771 mus musculus
10	8	3.9	586	5 Q9VEG2	Q9VEG2 drosophila
11	8	3.9	597	6 Q9TVD1	Q9TVD1 bos taurus
12	8	3.9	758	16 Q8DFQ8	Q8DFQ8 vibrrio vuln
13	8	3.9	758	16 Q87RD9	Q87RD9 vibrrio para
14	8	3.9	759	16 Q99TL6	Q99TL6 staphylococ
15	8	3.9	826	4 O00420	O00420 homo sapien
16	8	3.9	846	16 Q8XUK5	Q8XUK5 ralstonia s

17	8	3.9	846	16 Q8XPV0	Q8XPV0 ralstonia s
18	8	3.9	1743	5 Q9XWX5	Q9XWX5 caenorhabdi
19	7	3.4	62	5 Q26358	Q26358 onchocerca
20	7	3.4	78	11 Q9QY97	Q9QY97 rattus norv
21	7	3.4	102	5 Q9VUE1	Q9VUE1 drosophila
22	7	3.4	106	16 Q8NSZ6	Q8NSZ6 corynebacte
23	7	3.4	114	11 Q9CQH0	Q9CQH0 mus musculu
24	7	3.4	114	11 Q923S2	Q923S2 rattus norv
25	7	3.4	116	1 Q9UXM3	Q9UXM3 sulfolobus
26	7	3.4	116	12 Q69278	Q69278 equine herp
27	7	3.4	125	6 Q9N123	Q9N123 macaca fasc
28	7	3.4	132	5 Q9VQT9	Q9VQT9 drosophila
29	7	3.4	135	16 Q97H02	Q97H02 clostridium
30	7	3.4	136	5 Q86KR0	Q86KR0 dictyosteli
31	7	3.4	150	2 Q9F1P7	Q9F1P7 burkholderi
32	7	3.4	150	2 Q9ZF82	Q9ZF82 burkholderi
33	7	3.4	150	2 Q9LAN4	Q9LAN4 burkholderi
34	7	3.4	152	10 Q39738	Q39738 flaveria cr
35	7	3.4	159	3 Q14146	Q14146 schizosacch
36	7	3.4	162	10 Q39751	Q39751 flaveria pr
37	7	3.4	165	5 Q964Q0	Q964Q0 ixodes scap
38	7	3.4	173	17 Q9YC33	Q9YC33 aeropyrum p
39	7	3.4	178	17 Q9HIS3	Q9HIS3 thermoplas
40	7	3.4	193	10 Q84ZF1	Q84ZF1 oryza sativ
41	7	3.4	193	16 Q8NNQ1	Q8NNQ1 corynebacte
42	7	3.4	195	2 Q9ZHW7	Q9ZHW7 brucella me
43	7	3.4	202	16 Q69582	Q69582 mycobacteri
44	7	3.4	203	5 Q95YM3	Q95YM3 nippostro
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ALIGNMENTS

RESULT 1

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AC Q7Z7D2;
DT 01-OCT-2003 (TREMREL. 25, Created)
DT 01-OCT-2003 (TREMREL. 25, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Hepatocyte growth factor activator inhibitor 1B.
GN HAI1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kirchhofer D., Peek M., Li W., Stamos J., Eigenbrot C.,
RA Kadhodayan S., Elliott J.M., Corpuz R.T., Lazarus R.A., Moran P.;
RT "Tissue-expression, protease-specificity and Kunitz domain functions
of HAI-1B, a new splice variant of hepatocyte growth factor activator
inhibitor-1.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yuan J., Moran P.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY296715; AAP44001.1; -;
SQ SEQUENCE 529 AA; 58428 MW; B40F286C36D23437 CRC64;

Query Match 70.4%; Score 145; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 4.6e-150;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	384	FPSDKGHCVLDLPTGLCKESI PRWYNNPFSEHCARFTYGGCYGNKNFEEQQCLES CRG 443


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Db 444 ISKQVFGRLRREIPSTGSEVMAY 468

RESULT 2
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AC Q9D3K4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Serine protease inhibitor, kunitz type 1.
GN SPINT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017342; BAB30697.1; -.
DR HSSP; P05067; 1CA0.
DR MGD; MGI:1338033; Spint1.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002172; LDL_receptor_A.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; ldl_recept_a; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLa; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS0068; LDLRA_2; 1.
KW protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 507 AA; 56571 MW; 9EE0A29B7056D72D CRC64;

Query Match 19.4%; Score 40; DB 11; Length 507;
Best Local Similarity 100.0%; Pred. No. 6.8e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CARFTYGGCYGNKNFEEQQCLSCRGISKKDVFGRLRE 132
Db 394 CARFTYGGCYGNKNFEEQQCLSCRGISKKDVFGRLRE 433

RESULT 3
Q99J04
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Q99J04
Q99J04;
01-JUN-2001 (TReMBLrel. 17, Created)
01-JUN-2001 (TReMBLrel. 17, Last sequence update)
01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Serine protease inhibitor, kunitz type 1 (Spint1 protein).
GN SPINT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N-3; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N-3; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005769; AAH05769.1; -.
DR EMBL; BC053341; AAH53341.1; -.
DR HSSP; P05067; 1CA0.
DR MGD; MGI:1338033; Spint1.
DR GO; GO:0004867; F:peptidase activity; IEA.
DR GO; GO:0008233; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002172; LDL_receptor_A.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; ldl_recept_a; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLa; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS0068; LDLRA_2; 1.
KW Protease; Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 507 AA; 56590 MW; F7F9CCF2693D1F8D CRC64;

Query Match 19.4%; Score 40; DB 11; Length 507;
Best Local Similarity 100.0%; Pred. No. 6.8e-35;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CARFTYGGCYGNKNFEEQQCLSCRGISKKDVFGRLRE 132
Db 394 CARFTYGGCYGNKNFEEQQCLSCRGISKKDVFGRLRE 433
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RESULT 4
Q7XR48
ID Q7XR48 PRELIMINARY; PRT; 390 AA.
AC Q7XR48;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE OSJNBa0043A12.37 protein.
GN OSJNBa0043A12.37.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartioideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,
RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,
RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Peng Q.,
RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,
RA Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
RA Zhang R.Q., Guan J.P., Hong G.F.;
RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL606619; CAB02832.1; -.
SQ SEQUENCE 390 AA; 41437 MW; 8B9D170A780BF1FE CRC64;

Query Match 4.4%; Score 9; DB 10; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 HGHHPHP 181
Db 247 HGHHPHP 255

RESULT 5
Q8H2V9
ID Q8H2V9 PRELIMINARY; PRT; 250 AA.
AC Q8H2V9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE OSJNBb0011E04.11 protein.
GN OSJNBb0011E04.11.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartioideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
RT clone:OSJNBb0011E04.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005443; BAC22566.1; -.
SQ SEQUENCE 250 AA; 27639 MW; 60DA333BAD5822FF CRC64;

Query Match 3.9%; Score 8; DB 10; Length 250;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 PPPTPASS 186
Db 168 PPPTPASS 175

RESULT 6
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Q9NV85
ID Q9NV85 PRELIMINARY; PRT; 350 AA.
AC Q9NV85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ10874.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuho Y., Kanehori K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001736; BAA91870.1; -.
KW Hypothetical protein.
SQ SEQUENCE 350 AA; 39956 MW; D7B5875C34C9398C CRC64;

Query Match 3.9%; Score 8; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 MAVAVFLV 150
Db 78 MAVAVFLV 85

RESULT 7
Q9H813
ID Q9H813 PRELIMINARY; PRT; 350 AA.
AC Q9H813;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ14004.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK024066; BAB14810.1; -.
DR EMBL; BC006320; AAH06320.1; -.
KW Hypothetical protein.
SQ SEQUENCE 350 AA; 40043 MW; 5F68ACA21DDD0674 CRC64;

Query Match 3.9%; Score 8; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 MAVAVFLV 150
Db 78 MAVAVFLV 85
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RESULT 8

Q9CZV9 PRELIMINARY; PRT; 350 AA.
AC Q9CZV9; (Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 2310028N02Rik protein.
GN 2310028N02Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kačota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Carninci P., de Bonaldo M.F.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK012107; BAB28038.1; --
DR MGD; MGI:1914200; 2310028N02Rik.
SQ SEQUENCE 350 AA; 40285 MW; 12FD43319660775B CRC64;

Query Match 3.9%; Score 8; DB 11; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 MAVAVFLV 150

Db 78 MAVAVFLV 85

RESULT 9

Q9D771 PRELIMINARY; PRT; 350 AA.
AC Q9D771; (Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 2310028N02Rik protein (RIKEN cDNA 2310028N02 gene) (Hypothetical protein).
GN 2310028N02Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Carninci P., de Bonaldo M.F.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK009526; BAB26340.1; --
DR EMBL; BC027151; AAH27151.1; --
DR EMBL; AK031270; BAC27330.1; --
DR EMBL; AK044482; BAC31946.1; --
DR EMBL; AK049641; BAC33853.1; --
DR MGD; MGI:1914200; 2310028N02Rik.
KW Hypothetical protein.
SQ SEQUENCE 350 AA; 40178 MW; 3EE2CFBE929AE003 CRC64;

Query Match 3.9%; Score 8; DB 11; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 MAVAVFLV 150

Db 78 MAVAVFLV 85

RESULT 10

Q9VEG2 PRELIMINARY; PRT; 586 AA.
AC Q9VEG2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG16766 protein.
GN CG16766.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassaran D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupay J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Ciamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003719; AAF55462.2; -;
DR FlyBase; FBgn0038541; CG16766.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 586 AA; 64897 MW; BE89C75EE6B3844F CRC64;
Query Match 3.9%; Score 8; DB 5; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 144 AVAVFLVI 151
Db 77 AVAVFLVI 84
RESULT 11
Q9TVD1
ID Q9TVD1 PRELIMINARY; PRT; 597 AA.
AC Q9TVD1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Dopamine beta-hydroxylase precursor.
GN DBH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal medulla;
RX MEDLINE=90285664; PubMed=1693949;
RA Wu H.J., Farmer R.J., Koop A.H., Rozansky D.J., O'Connor D.T.;
RT "Molecular cloning, structure, and expression of dopamine beta-hydroxylase from bovine adrenal medulla.";
RL J. Neurochem. 55:97-105(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal medulla;
RA Wu H.J., Farmer R.J., Koop A.H., Rozansky D.J., O'Connor D.T.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF118638; AAD09829.1; -;
DR HSSP; P14925; 1PHM.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0004500; F:dopamine beta-monooxygenase activity; IEA.
DR GO; GO:0006584; P:catecholamine metabolism; IEA.
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR000945; DB_monooxygenase.
DR InterPro; IPR005018; DOMON.
DR InterPro; IPR008977; PHM_PNGase_F.
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF03712; Cu2_monoox_C; 1.
DR Pfam; PF03351; DOMON; 1.
DR PRINTS; PR00767; DBMONOXGNASE.
DR SMART; SM00664; Doh; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
DR PROSITE; PS00085; CU2_MONOOXYGENASE_2; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 597 DOPAMINE BETA-HYDROXYLASE.
SQ SEQUENCE 597 AA; 66685 MW; CF89D62A9472B7C6 CRC64;
Query Match 3.9%; Score 8; DB 6; Length 597;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 144 AVAVFLVI 151
Db 5 AVAVFLVI 12
RESULT 12

Q8DFQ8
 ID Q8DFQ8 PRELIMINARY; PRT; 758 AA.
 AC Q8DFQ8;
 DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Fe2+ transport system protein B.
 GN VV10148.
 OS Vibrio vulnificus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 CX NCBI_TaxID=672;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choy H.E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE016797; AAO08686.1; -
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015093; F:ferrous iron transporter activity; IEA.
 DR GO; GO:0015684; P:ferrous iron transport; IEA.
 DR InterPro; IPR003373; FeoB.
 DR InterPro; IPR006073; GTP1_OBG.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF02421; FeoB; 1.
 DR PRINTS; PR00326; GTP1_OBG.
 DR TIGRFAMS; TIGR00437; feoB; 1.
 DR TIGRFAMS; TIGR00231; small_GTP; 1.
 KW Complete proteome.
 SQ SEQUENCE 758 AA; 82450 MW; 3ABE99077B86A57D CRC64;
 Query Match 3.9%; Score 8; DB 16; Length 758;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 153 IVVVVAIL 160
 DB 516 IVVVVAIL 523

RESULT 13
 Q87RD9
 ID Q87RD9 PRELIMINARY; PRT; 758 AA.
 AC Q87RD9;
 DT 01-JUN-2003 (TREMELrel. 24, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Ferrous iron transport protein B.
 GN VP0858.
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 CX NCBI_TaxID=670;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RIMD 2210633 / Serotype O3:K6;
 RX MEDLINE=22508454; PubMed=12620739;
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Nishijima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RT "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism
 distinct from that of *V. cholerae*.";
 RL Lancet 361:743-749 (2003).
 DR EMBL; AP005075; BAC59121.1; -
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015093; F:ferrous iron transporter activity; IEA.
 DR GO; GO:0015684; P:ferrous iron transport; IEA.
 DR InterPro; IPR003373; FeoB.
 DR InterPro; IPR006073; GTP1_OBG.
 DR Pfam; PF02421; FeoB; 1.
 DR PRINTS; PR00326; GTP1_OBG.

QY 153 IVVVVAIL 160
 DB 516 IVVVVAIL 523

RESULT 14
 Q99TL6
 ID Q99TL6 PRELIMINARY; PRT; 759 AA.
 AC Q99TL6;
 DT 01-JUN-2001 (TREMELrel. 17, Created)
 DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Protein-export membrane protein SecDF.
 GN SECF OR SAV1637 OR SA1463 OR MW1587.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
 OS Staphylococcus aureus (strain N315), and
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=158878, 158879, 196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mu50, and N315;
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
aureus.";
 RL Lancet 357:1225-1240 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 acquired MRSA.";
 RL Lancet 359:1819-1827 (2002).
 DR EMBL; AP003363; BAB57799.1; -
 DR EMBL; AP003134; BAB42729.1; -
 DR EMBL; AP004827; BAB95452.1; -
 DR PIR; D89946; D89946.
 DR GO; GO:0019866; C:inner membrane; IEA.
 DR GO; GO:0015627; C:type II protein secretion system complex; IEA.
 DR GO; GO:0015450; F:protein translocase activity; IEA.
 DR GO; GO:0006886; P:intracellular protein transport; IEA.
 DR GO; GO:0015628; P:type II protein (Sec) secretion system; IEA.
 DR InterPro; IPR005791; SecD.
 DR InterPro; IPR003335; SecD_SecF.
 DR Pfam; PF02355; SecD_SecF; 1.
 DR PRINTS; PR01755; SECFTRNLCASE.
 DR TIGRFAMS; TIGR00916; 2A0604s01; 2.
 DR TIGRFAMS; TIGR01129; secD; 1.
 KW Complete proteome.
 SQ SEQUENCE 759 AA; 84253 MW; 7E6B8BAC0D24BF47 CRC64;
 Query Match 3.9%; Score 8; DB 16; Length 759;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 153 IVVVVAIL 160

Db 688 IVWVAIL 695

RESULT 15
O00420
ID O00420 PRELIMINARY; PRT: 826 AA.
AC O00420;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F19541_1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Adamson A.A., Burkhardt-Schultz K.,
RA Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan L.,
RA Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
RT "Sequence analysis of a 1 Mb region in human 19q13.1.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U95090; AAB80768.1; --
DR Genew; HGNC:17325; PRODH2.
DR GO; GO:0004657; F:proline dehydrogenase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006537; P:glutamate biosynthesis; IEA.
DR GO; GO:0006562; P:proline catabolism; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000209; Peptidase_S8.
DR InterPro; IPR002872; Pro_dh.
DR Pfam; PF01619; Pro_dh; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
FT NON TER 1
SQ SEQUENCE 826 AA; 90814 MW; 25CED0CB6970072E CRC64;

Query Match 3.9%; Score 8; DB 4; Length 826;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 185 SSTVSTTE 192
Db 74 SSTVSTTE 81

Search completed: April 22, 2004, 10:25:16
Job time : 68 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 09:32:14 ; Search time 18 Seconds
(without alignments)
595.914 Million cell updates/sec

Title: US-09-935-390A-23
Perfect score: 206
Sequence: 1 MERRHPVCSGTCQPTQFRCS.....TVSTTEDTEHLVYNHTTRPL 206

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	513	1 SPT1_HUMAN	O43278 homo sapien
2	40	19.4	507	1 SPT1_MOUSE	Q9r097 mus musculus
3	11	5.3	4660	1 LRP2_RAT	P98158 rattus norv
4	8	3.9	610	1 DOPO_BOVIN	P15101 bos taurus
5	8	3.9	1241	1 NPHN_HUMAN	O60500 homo sapien
6	7	3.4	90	1 Y58S_ARCFU	O29670 archaeoglob
7	7	3.4	114	1 MA17_HUMAN	Q13113 homo sapien
8	7	3.4	147	1 RZPR_ECOLI	P77551 escherichia
9	7	3.4	242	1 APL_LACLC	Q48630 lactococcus
10	7	3.4	354	1 CAHC_HUMAN	O43570 homo sapien
11	7	3.4	387	1 QIN_AVIS3	P56260 avian sarco
12	7	3.4	436	1 BRNQ_HAEIN	P71345 haemophilus
13	7	3.4	451	1 FXGB_CHICK	Q90964 gallus gall
14	7	3.4	469	1 FXGA_HUMAN	P55316 homo sapien
15	7	3.4	477	1 FXGB_HUMAN	P55315 homo sapien
16	7	3.4	480	1 FXGB_RAT	Q00939 rattus norv
17	7	3.4	481	1 FXGB_MOUSE	Q60987 mus musculus
18	7	3.4	482	1 K6B2_HUMAN	Q9ubs0 h ribosomal
19	7	3.4	485	1 K6B2_MOUSE	Q921m4 mus musculus
20	7	3.4	502	1 K6B1_HUMAN	P23443 homo sapien
21	7	3.4	502	1 K6B1_RAT	P21425 rattus norv
22	7	3.4	510	1 HYAP_MACFA	P38568 macaca fasc
23	7	3.4	671	1 NCPR_MUSDO	Q07994 musca domes
24	7	3.4	672	1 SL52_HUMAN	P31639 homo sapien
25	7	3.4	902	1 NFC4_HUMAN	Q14934 homo sapien
26	7	3.4	950	1 KCH6_RAT	O54853 rattus norv
27	7	3.4	994	1 KCH6_HUMAN	Q9h252 homo sapien
28	7	3.4	994	1 PPOL_DROME	P35875 drosophila
29	7	3.4	1033	1 ACAC_ARATH	Q9ly77 arabidopsis
30	7	3.4	1158	1 KCH2_CANFA	Q9tsz3 canis famil
31	7	3.4	1159	1 KCH2_HUMAN	Q12809 homo sapien
32	7	3.4	1161	1 KCH2_RABIT	Q8wny2 oryctolagus
33	7	3.4	1162	1 KCH2_MOUSE	O35219 mus musculus

34	7	3.4	1163	1 KCH2_RAT	O08962 rattus norv
35	7	3.4	1733	1 VNUA_PRVKA	P33485 pseudorabie
36	7	3.4	2505	1 CCAA_HUMAN	O00555 homo sapien
37	6	2.9	45	1 VNSX_CVBM	P22052 bovine coro
38	6	2.9	53	1 HTIB_MANSE	P26227 manduca sex
39	6	2.9	58	1 AXPI_ANTAF	P81547 anthopleura
40	6	2.9	67	1 IBPC_BOVIN	P00976 bos taurus
41	6	2.9	73	1 PSBH_MESVI	Q9mu44 mesostigma
42	6	2.9	77	1 CVP6_PIMHY	Q8t0w0 pimpla hypo
43	6	2.9	79	1 PSBH_CHLVU	P56323 chlorella v
44	6	2.9	81	1 PN3C_PENVA	P81060 penaeus van
45	6	2.9	81	1 PN3J_PENVA	Q963d9 penaeus van

ALIGNMENTS

RESULT 1
SPT1_HUMAN
ID SPT1_HUMAN STANDARD; PRT; 513 AA.
AC O43278;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor
DE activator inhibitor type 1) (HAI-1).
GN SPINT1 OR HAI1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97197808; PubMed=9045658;
RA Shimomura T., Denda K., Kitamura A., Kawaguchi T., Kito M., Kondo J.,
RA Kagaya S., Qin L., Takata H., Miyazawa K., Kitamura N.;
RT "Hepatocyte growth factor activator inhibitor, a novel Kunitz-type
RT serine protease inhibitor."
RL J. Biol. Chem. 272:6370-6376(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Placenta;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatlenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC TISSUE=Milk;
RX MEDLINE=99303582; PubMed=10373425;
RA Lin C.Y., Anders J., Johnson M., Dickson R.B.;
RT "Purification and characterization of a complex containing matrilase
RT and a Kunitz-type serine protease inhibitor from human milk."
RL J. Biol. Chem. 274:18237-18242(1999).
CC -!- FUNCTION: Inhibitor of HGF activator. Also acts as an inhibitor of
CC matrilase (ST14).

OY 93 CARFTYGGCYGNKNFEEQQCLESCRGISKKDVFGLRRE 132
|||||
Db 394 CARFTYGGCYGNKNFEEQQCLESCRGISKKDVFGLRRE 433

RESULT 3

LRP2_RAT
ID_LRP2_RAT STANDARD; PRT; 4660 AA.
AC P98158;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE low-density lipoprotein receptor-related protein 2 precursor (Megalin)
DE (Glycoprotein 330) (gp330).
GN LRP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RF SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=95024033; PubMed=7937880;
RA Saito A., Pietromonaco S., Loo A.K.C., Farquhar M.G.;
RT "Complete cloning and sequencing of rat gp330/megalin," a
RT distinctive member of the low density lipoprotein receptor gene
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729(1994).
RN [2]
RF FUNCTION.
RX MEDLINE=95386696; PubMed=7544804;
RA Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.B.,
RA Norris K., Gliemann J., Christensen B.I.;
RT "Evidence that epithelial glycoprotein 330/megalin mediates uptake of
RT polybasic drugs.";
RL J. Clin. Invest. 96:1404-1413(1995).
RN [3]
RF TISSUE SPECIFICITY.
RX MEDLINE=94172242; PubMed=7510321;
RA Zheng G., Bachinsky D.R., Stamenkovic I., Strickland D.K., Brown D.,
RA Andres G., McCluskey R.T.;
RT "Organ distribution in rats of two members of the low-density
RT lipoprotein receptor gene family, gp330 and LRP/alpha 2MR, and the
RT receptor-associated protein (RAP).";
RL J. Histochem. Cytochem. 42:531-542(1994).
CC -!- FUNCTION: Binds plasminogen, extracellular matrix components,
CC plasminogen activator-plasminogen activator inhibitor type I
CC complex, apolipoprotein B-enriched beta-VLDL, lipoprotein lipase,
CC lactoferrin, clusterin and calcium.
CC -!- FUNCTION: Receptor-mediated uptake of polybasic drugs such as
CC aprotinin, aminoglycosides and polymyxin B.
CC -!- SUBUNIT: Forms a multimeric complex together with a receptor-
CC associated protein (RAP). Binds to ankyrin-repeat family A protein
CC 2 (ANKRA2) (5y similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Expressed in
CC clathrin-coated pits; a soluble form is possibly derived by
CC cleavage at the cell surface.
CC -!- TISSUE SPECIFICITY: Epithelial cells of kidney glomerulus and
CC proximal tubule, lung, epididymis, yolk sac, among others.
CC -!- SIMILARITY: Contains 36 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 37 LDL-receptor class B domains.
CC -!- SIMILARITY: Contains 17 EGF-like domains.
CC -----
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CC -----
CC EMBL; L34049; AAA51369.1; -.

DR PIR; T42737; T42737.
DR HSP; Q07954; ICR8.
DR GlycoSuiteDB; P98158;
DR InterPro; IPR000152; Asx_hydroxyl_s.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000033; Ldl_receptor_rep.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00057; ldl_recept_a; 36.
DR Pfam; PF00058; ldl_recept_b; 33.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00192; LDLa; 36.
DR SMART; SM00135; LY; 34.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS50026; EGF_3; 8.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS01209; LDLRA_1; 31.
DR PROSITE; PS50068; LDLRA_2; 36.
KW Glycoprotein; Repeat; Endocytosis; Coated pits; Transmembrane;
KW Receptor; EGF-like domain; SH3-binding; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 4660 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
FT PROTEIN 2.
FT DOMAIN 26 4425 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 4426 4446 POTENTIAL.
FT DOMAIN 4447 4660 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 64 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 65 105 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 106 144 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 145 181 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 181 219 LDL-RECEPTOR CLASS A 5.
FT DOMAIN 220 258 LDL-RECEPTOR CLASS A 6.
FT DOMAIN 263 307 LDL-RECEPTOR CLASS A 7.
FT DOMAIN 308 346 EGF-LIKE 1.
FT DOMAIN 347 385 EGF-LIKE 2.
FT DOMAIN 435 476 LDL-RECEPTOR CLASS B 1.
FT DOMAIN 478 519 LDL-RECEPTOR CLASS B 2.
FT DOMAIN 521 566 LDL-RECEPTOR CLASS B 3.
FT DOMAIN 568 611 LDL-RECEPTOR CLASS B 4.
FT DOMAIN 612 652 LDL-RECEPTOR CLASS B 5.
FT DOMAIN 658 704 EGF-LIKE 3.
FT DOMAIN 752 793 LDL-RECEPTOR CLASS B 6.
FT DOMAIN 795 835 LDL-RECEPTOR CLASS B 7.
FT DOMAIN 837 879 LDL-RECEPTOR CLASS B 8.
FT DOMAIN 881 923 LDL-RECEPTOR CLASS B 9.
FT DOMAIN 969 1013 EGF-LIKE 4.
FT DOMAIN 1023 1061 LDL-RECEPTOR CLASS A 8.
FT DOMAIN 1064 1103 LDL-RECEPTOR CLASS A 9.
FT DOMAIN 1108 1146 LDL-RECEPTOR CLASS A 10.
FT DOMAIN 1148 1186 LDL-RECEPTOR CLASS A 11.
FT DOMAIN 1186 1225 LDL-RECEPTOR CLASS A 12.
FT DOMAIN 1229 1269 LDL-RECEPTOR CLASS A 13.
FT DOMAIN 1270 1308 LDL-RECEPTOR CLASS A 14.
FT DOMAIN 1311 1351 LDL-RECEPTOR CLASS A 15.
FT DOMAIN 1350 1390 EGF-LIKE 5.
FT DOMAIN 1391 1430 EGF-LIKE 6. CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1479 1520 LDL-RECEPTOR CLASS B 10.
FT DOMAIN 1522 1563 LDL-RECEPTOR CLASS B 11.
FT DOMAIN 1567 1609 LDL-RECEPTOR CLASS B 12.
FT DOMAIN 1611 1654 LDL-RECEPTOR CLASS B 13.
FT DOMAIN 1656 1696 LDL-RECEPTOR CLASS B 14.
FT DOMAIN 1701 1742 EGF-LIKE 7.
FT DOMAIN 1791 1832 LDL-RECEPTOR CLASS B 15.
FT DOMAIN 1834 1882 LDL-RECEPTOR CLASS B 16.
FT DOMAIN 1884 1930 LDL-RECEPTOR CLASS B 17.
FT DOMAIN 1932 1972 LDL-RECEPTOR CLASS B 18.
FT DOMAIN 1973 2013 LDL-RECEPTOR CLASS B 19.
FT DOMAIN 2019 2060 EGF-LIKE 8.
FT DOMAIN 2108 2156 LDL-RECEPTOR CLASS B 20.

FT	DOMAIN	2158	2201	LDL-RECEPTOR	CLASS B 21.
FT	DOMAIN	2203	2245	LDL-RECEPTOR	CLASS B 22.
FT	DOMAIN	2247	2289	LDL-RECEPTOR	CLASS B 23.
FT	DOMAIN	2291	2332	LDL-RECEPTOR	CLASS B 24.
FT	DOMAIN	2343	2384	EGF-LIKE 9.	
FT	DOMAIN	2432	2477	LDL-RECEPTOR	CLASS B 25.
FT	DOMAIN	2479	2518	LDL-RECEPTOR	CLASS B 26.
FT	DOMAIN	2520	2562	LDL-RECEPTOR	CLASS B 27.
FT	DOMAIN	2564	2604	LDL-RECEPTOR	CLASS B 28.
FT	DOMAIN	2605	2647	LDL-RECEPTOR	CLASS B 29.
FT	DOMAIN	2652	2694	EGF-LIKE 10.	
FT	DOMAIN	2699	2739	LDL-RECEPTOR	CLASS A 16.
FT	DOMAIN	2740	2778	LDL-RECEPTOR	CLASS A 17.
FT	DOMAIN	2779	2820	LDL-RECEPTOR	CLASS A 18.
FT	DOMAIN	2821	2862	LDL-RECEPTOR	CLASS A 19.
FT	DOMAIN	2863	2903	LDL-RECEPTOR	CLASS A 20.
FT	DOMAIN	2906	2947	LDL-RECEPTOR	CLASS A 21.
FT	DOMAIN	2948	2992	LDL-RECEPTOR	CLASS A 22.
FT	DOMAIN	2993	3031	LDL-RECEPTOR	CLASS A 23.
FT	DOMAIN	3032	3072	LDL-RECEPTOR	CLASS A 24.
FT	DOMAIN	3075	3112	LDL-RECEPTOR	CLASS A 25.
FT	DOMAIN	3113	3153	EGF-LIKE 11.	
FT	DOMAIN	3154	3194	EGF-LIKE 12.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	3241	3282	LDL-RECEPTOR	CLASS B 30.
FT	DOMAIN	3284	3333	LDL-RECEPTOR	CLASS B 31.
FT	DOMAIN	3335	3377	LDL-RECEPTOR	CLASS B 32.
FT	DOMAIN	3379	3420	LDL-RECEPTOR	CLASS B 33.
FT	DOMAIN	3421	3461	LDL-RECEPTOR	CLASS B 34.
FT	DOMAIN	3467	3511	EGF-LIKE 13.	
FT	DOMAIN	3512	3552	LDL-RECEPTOR	CLASS A 26.
FT	DOMAIN	3553	3593	LDL-RECEPTOR	CLASS A 27.
FT	DOMAIN	3594	3634	LDL-RECEPTOR	CLASS A 28.
FT	DOMAIN	3635	3675	LDL-RECEPTOR	CLASS A 29.
FT	DOMAIN	3678	3718	LDL-RECEPTOR	CLASS A 30.
FT	DOMAIN	3719	3758	LDL-RECEPTOR	CLASS A 31.
FT	DOMAIN	3759	3797	LDL-RECEPTOR	CLASS A 32.
FT	DOMAIN	3798	3836	LDL-RECEPTOR	CLASS A 33.
FT	DOMAIN	3842	3882	LDL-RECEPTOR	CLASS A 34.
FT	DOMAIN	3883	3924	LDL-RECEPTOR	CLASS A 35.
FT	DOMAIN	3928	3966	LDL-RECEPTOR	CLASS A 36.
FT	DOMAIN	3968	4008	EGF-LIKE 14.	
FT	DOMAIN	4009	4050	EGF-LIKE 15.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	4156	4197	LDL-RECEPTOR	CLASS B 35.
FT	DOMAIN	4199	4241	LDL-RECEPTOR	CLASS B 36.
FT	DOMAIN	4244	4284	LDL-RECEPTOR	CLASS B 37.
FT	DOMAIN	4332	4370	EGF-LIKE 16.	
FT	DOMAIN	4379	4413	EGF-LIKE 17.	
FT	SITE	4454	4460	SH3-BINDING (POTENTIAL).	
FT	SITE	4457	4463	SH3-BINDING (POTENTIAL).	
FT	SITE	4606	4609	SH2-BINDING (POTENTIAL).	
FT	SITE	4619	4625	SH3-BINDING (POTENTIAL).	
FT	SITE	4624	4630	SH3-BINDING (POTENTIAL).	
FT	SITE	1743	1745	CELL ATTACHMENT SITE (POTENTIAL).	
FT	SITE	4522	4527	ENDOCYTOSIS SIGNAL (POTENTIAL).	
FT	SITE	4601	4606	ENDOCYTOSIS SIGNAL (POTENTIAL).	
FT	DISULFID	28	40	BY SIMILARITY.	
FT	DISULFID	35	53	BY SIMILARITY.	
FT	DISULFID	47	62	BY SIMILARITY.	
FT	DISULFID	67	80	BY SIMILARITY.	
FT	DISULFID	74	93	BY SIMILARITY.	
FT	DISULFID	87	103	BY SIMILARITY.	
FT	DISULFID	108	120	BY SIMILARITY.	

Query Match 5.3%; Score 11; DB 1; Length 4660;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 SGTCQPTQFRC 19
| | | | |
Db 1147 SGTCQPTQFRC 1157

RESULT 4

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DOPO BOVIN
ID DOPO BOVIN STANDARD; PRT; 610 AA.
AC P15101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dopamine beta-monooxygenase precursor (EC 1.14.17.1) (Dopamine beta-hydroxylase) (DBH).
GN DBH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90148928; PubMed=2620060;
RA Taljanidisz J., Stewart L., Smith A.J., Klinman J.P.;
RT "Structure of bovine adrenal dopamine beta-monooxygenase, as deduced from cDNA and protein sequencing: evidence that the membrane-bound form of the enzyme is anchored by an uncleaved signal peptide.";
RL Biochemistry 28:10054-10061(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90110081; PubMed=1688549;
RA Lewis E.J., Allison S., Fader D., Claflin V., Baizer L.;
RT "Bovine dopamine beta-hydroxylase cDNA. Complete coding sequence and expression in mammalian cells with vaccinia virus vector.";
RL J. Biol. Chem. 265:1021-1028(1990).
RN [3]
RP PARTIAL SEQUENCE OF 33-610.
RX MEDLINE=90110082; PubMed=22955597;
RA Robertson J.G., Desai P.R., Kumar A., Farrington G.K., Fitzpatrick P.P., Villafranca J.J.;
RT "Primary amino acid sequence of bovine dopamine beta-hydroxylase.";
RL J. Biol. Chem. 265:1029-1035(1990).
RN [4]
RP SEQUENCE OF 33-50.
RX TISSUE=Adrenal medulla;
RX MEDLINE=77134133; PubMed=8433373;
RA Skotland T., Ljones T., Flatmark T., Sletten K.;
RT "NH2-terminal sequence of dopamine beta-hydroxylase from bovine adrenal medulla.";
RL Biochem. Biophys. Res. Commun. 74:1483-1489(1977).
RN [5]
RP SEQUENCE OF 33-37.
RX MEDLINE=89079641; PubMed=2909511;
RA Taylor C.S., Kent U.M., Fleming P.J.;
RT "The membrane-binding segment of dopamine beta-hydroxylase is not an uncleaved signal sequence.";
RL J. Biol. Chem. 264:14-16(1989).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=95001861; PubMed=7918370;
RA Robertson J.G., Adams G.W., Medzihradsky K.F., Burlingame A.L., Villafranca J.J.;
RT "Complete assignment of disulfide bonds in bovine dopamine beta-hydroxylase.";
RL Biochemistry 33:11563-11575(1994).
CC -!- FUNCTION: Conversion of dopamine to noradrenaline.
CC -!- CATALYTIC ACTIVITY: 3,4-dihydroxyphenethylamine + ascorbate + O(2) = noradrenaline + dehydroascorbate + H(2)O.
CC -!- COFACTOR: PQQ, copper and ascorbate.
CC -!- PATHWAY: Catecholamine biosynthesis.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Exists both in a soluble form (in chromaffin granules) and as membrane bound (the membrane bound form is anchored by an uncleaved signal peptide).
CC -!- SIMILARITY: Belongs to the copper type II, ascorbate-dependent monooxygenase family.
CC -!- SIMILARITY: Contains 1 DOMON domain.
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DR EMBL; J02890; AAA30356.1; --
DR EMBL; J05160; AAA30490.1; ALT_INIT.
DR HSSP; P14925; 1PHM.
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR000945; DB_monooxygenase.
DR InterPro; IPR005018; DOMON.
DR InterPro; IPR008977; PHM_PNGase_F.
DR Pfam; PF03712; Cu2_monooxygen; 1.
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF03351; DOMON; 1.
DR PRINTS; PR00767; DEMONOXGNASE.
DR SMART; SM00664; DoH; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
DR PROSITE; PS00085; CU2_MONOOXYGENASE_2; 1.
DR PROSITE; PS50836; DOMON; 1.
KW Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Copper;
KW Vitamin C; PQQ; Glycoprotein; Membrane; Signal.
FT SIGNAL 1 32
FT CHAIN 33 610 DOPAMINE BETA-MONOOXYGENASE.
FT DOMAIN 50 166 DOMON.
FT ACT_SITE 223 223
FT ACT_SITE 405 405 POTENTIAL.
FT METAL 405 405 COPPER (POTENTIAL).
FT DISULFID 147 589
FT DISULFID 225 276
FT DISULFID 262 288
FT DISULFID 383 496
FT DISULFID 387 558
FT DISULFID 459 481
FT DISULFID 521 521 INTERCHAIN.
FT DISULFID 523 523 INTERCHAIN.
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .).
FT CARBOHYD 559 559 N-LINKED (GLCNAC. . .).
FT CONFLICT 35 35 P -> T (IN REF. 4).
FT CONFLICT 48 48 P -> T (IN REF. 4).
FT CONFLICT 55 57 SWN -> RYV (IN REF. 3).
FT CONFLICT 74 74 L -> F (IN REF. 3).
FT CONFLICT 205 205 C -> R (IN REF. 2).
FT CONFLICT 267 269 RDH -> ETI (IN REF. 2).
FT CONFLICT 560 560 R -> C (IN REF. 3).
FT CONFLICT 588 588 Q -> H (IN REF. 2).
SQ SEQUENCE 610 AA; 68143 MW; 1639DB670F94DE71 CRC64;

Query Match 3.9%; Score 8; DB 1; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 AVAVFLVI 151
Db 18 AVAVFLVI 25
|||||

RESULT 5
NPEN HUMAN STANDARD; PRT; 1241 AA.
AC O60500;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nephtrin precursor (Renal glomerulus-specific cell adhesion receptor).
GN NPHS1 OR NPHN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98325371; PubMed=9660941;
RA Kestilae M., Lenkkeri U., Maennikkoe M., Lamerdin J., McCready P.,
RA Putaala H., Ruotsalainen V., Morita T., Nissinen M., Herva R.,
RA Kashtan C.E., Peltonen L., Holmberg C., Olsen A., Tryggvason K.;
RT "Positionally cloned gene for a novel glomerular protein -- nephrin --
RT is mutated in congenital nephrotic syndrome.";
RL Mol. Cell 1:575-582(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Grunkemeyer J.A., Kumar N., Kalluri R.;
RT "Human nephrin (NPHS1) cDNA sequence.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1032-1134 FROM N.A. (ISOFORM 2), AND SUBCELLULAR LOCATION.
RX MEDLINE=20019662; PubMed=10550324;
RA Holthoefer H., Ahola H., Solin M.-L., Wang S.-X., Palmen T.,
RA Luimula P., Miettinen A., Kerjaschki D.;
RT "Nephrin localizes at the podocyte filtration slit area and is
RT characteristically spliced in the human kidney.";
RL Am. J. Pathol. 155:1681-1687(1999).
RN [4]
RP SUBCELLULAR LOCATION.
RX MEDLINE=99324171; PubMed=10393930;
RA Ruotsalainen V., Ljungberg P., Wartiovaara J., Lenkkeri U.,
RA Kestilae M., Jalanko H., Holmberg C., Tryggvason K.;
RT "Nephrin is specifically located at the slit diaphragm of glomerular
RT podocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:7962-7967(1999).
RN [5]
RP INTERACTION WITH NPHS2.
RX MEDLINE=21551283; PubMed=11562357;
RA Huber T.B., Kottgen M., Schilling B., Walz G., Benzing T.;
RT "Interaction with podocin facilitates nephrin signaling.";
RL J. Biol. Chem. 276:41543-41546(2001).
RN [6]
RP VARIANTS LYS-117 AND SER-1077, AND VARIANTS CNP SER-64; ASN-171;
RP THR-172 DEL; ASN-173; 205-THR--ARG-207 DELINS ILE; CYS-270;
RP PRO-350; ARG-366; CYS-367; SER-368; VAL-376; GLN-408; TYR-465;
RP PHE-528; GLN-610; PHE-623; CYS-724; CYS-743; TRP-802; PRO-802;
RP ASP-806; CYS-831 AND CYS-1140.
RX MEDLINE=99115081; PubMed=9915943;
RA Lenkkeri U., Maennikkoe M., McCready P., Lamerdin J., Gribouval O.,
RA Naudet P.M., Antignac C.K., Kashtan C.E., Olsen A.,
RA Kestilae M., Tryggvason K.;
RT "Structure of the gene for congenital nephrotic syndrome of the
RT Finnish type (NPHS1) and characterization of mutations.";
RL Am. J. Hum. Genet. 64:51-61(1999).
RN [7]
RP VARIANTS CNP LYS-447 AND VAL-819.
RX MEDLINE=20117947; PubMed=10652016;
RA Aya K., Tanaka H., Seino Y.;
RT "Novel mutation in the nephrin gene of a Japanese patient with
RT congenital nephrotic syndrome of the Finnish type.";
RL Kidney Int. 57:401-404(2000).
CC -!- FUNCTION: Seems to play a role in the development or function of
CC the kidney glomerular filtration barrier. May anchor the podocyte
CC slit diaphragm to the actin cytoskeleton.
CC -!- SUBUNIT: Interacts with podocin/NPHS2. Interacts with CD2AP C-
CC terminal domain (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC Predominantly located at podocyte slit diaphragm between podocyte
CC foot processes. Also associated with podocyte apical plasma
CC membrane.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O60500-1; Sequence=Displayed;
CC Name=2; Synonyms=Alpha;
CC IsoId=O60500-2; Sequence=VSP_002598;
CC -!- TISSUE SPECIFICITY: Specifically expressed in podocytes of kidney
CC glomeruli.
CC -!- DEVELOPMENTAL STAGE: In 23-week-old embryo found in epithelial

CC podocytes of the periphery of mature and developing glomeruli.
CC -!- PTM: Phosphorylated on tyrosine residues.
CC -!- DISEASE: Defects in NPHS1 are the cause of congenital nephrotic
CC syndrome of the Finnish type (NPHS1 or CNP) [MIM:256300]; an
CC autosomal recessive disorder characterized by massive proteinuria
CC in utero and nephrosis at birth.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -!- SIMILARITY: Contains 8 immunoglobulin-like domains.
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CC -----
DR EMBL; AF035835; AAC39687.1; -.
DR EMBL; AF190637; AAG17141.1; -.
DR EMBL; AF126957; AAF36451.1; -.
DR PIR; T37190; T37190.
DR Genew; HGNC:7908; NPHS1.
DR MIM; 602716; -.
DR MIM; 256300; -.
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0007155; P: cell adhesion; TAS.
DR GO; GO:0007588; P: excretion; TAS.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 8.
DR SMART; SMO0060; FN3; 1.
DR SMART; SMO0408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 7.
KW Cell adhesion; Transmembrane; Signal; Glycoprotein;
KW Immunoglobulin domain; Repeat; Phosphorylation; Alternative splicing;
KW Disease mutation; Polymorphism.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 1241 NEPHRIN.
FT DOMAIN 23 1055 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1056 1076 POTENTIAL.
FT DOMAIN 1077 1241 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 130 IG-LIKE C2-TYPE 1.
FT DOMAIN 143 234 IG-LIKE C2-TYPE 2.
FT DOMAIN 242 333 IG-LIKE C2-TYPE 3.
FT DOMAIN 340 434 IG-LIKE C2-TYPE 4.
FT DOMAIN 440 540 IG-LIKE C2-TYPE 5.
FT DOMAIN 544 635 IG-LIKE C2-TYPE 6.
FT DOMAIN 740 832 IG-LIKE C2-TYPE 7.
FT DOMAIN 838 939 IG-LIKE C2-TYPE 8.
FT DOMAIN 941 1025 FIBRONECTIN TYPE-III.
FT DOMAIN 1160 1241 BINDS TO NPHS2.
FT DISULFID 53 111 POTENTIAL.
FT DISULFID 160 217 POTENTIAL.
FT DISULFID 265 317 POTENTIAL.
FT DISULFID 361 417 POTENTIAL.
FT DISULFID 465 528 POTENTIAL.
FT DISULFID 567 623 POTENTIAL.
FT DISULFID 761 816 POTENTIAL.
FT DISULFID 863 920 POTENTIAL.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 547 547 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 680 680 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 708 708 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 908 908 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	VARSPLIC	1056	1095	Missing (in isoform 2). /FTid=VSP 002598. W -> S (IN CNF). /FTid=VAR_013029. E -> K. /FTid=VAR_013030. I -> N (IN CNF). /FTid=VAR_013031. MISSING (IN CNF). /FTid=VAR_013032. I -> N (IN CNF). /FTid=VAR_013033. TPR -> I (IN CNF). /FTid=VAR_013034. G -> C (IN CNF). /FTid=VAR_013035. S -> P (IN CNF). /FTid=VAR_013036. S -> R (IN CNF). /FTid=VAR_013037. R -> C (IN CNF). /FTid=VAR_013038. P -> S (IN CNF). /FTid=VAR_013039. L -> V (IN CNF). /FTid=VAR_013040. R -> Q (IN CNF; COULD BE A POLYMORPHISM). /FTid=VAR_013041. E -> K (IN CNF). /FTid=VAR_013042. C -> Y (IN CNF). /FTid=VAR_013043. C -> F (IN CNF). /FTid=VAR_013044. L -> Q (IN CNF). /FTid=VAR_013045. C -> F (IN CNF). /FTid=VAR_013046. S -> C (IN CNF). /FTid=VAR_013047. R -> C (IN CNF). /FTid=VAR_013048.
FT	VARIANT	64	64	
FT	VARIANT	117	117	
FT	VARIANT	171	171	
FT	VARIANT	172	172	
FT	VARIANT	173	173	
FT	VARIANT	205	207	
FT	VARIANT	270	270	
FT	VARIANT	350	350	
FT	VARIANT	366	366	
FT	VARIANT	367	367	
FT	VARIANT	368	368	
FT	VARIANT	376	376	
FT	VARIANT	408	408	
FT	VARIANT	447	447	
FT	VARIANT	465	465	
FT	VARIANT	528	528	
FT	VARIANT	610	610	
FT	VARIANT	623	623	
FT	VARIANT	724	724	
FT	VARIANT	743	743	

Query Match 3.9%; Score 8; DB 1; Length 1241;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 SSTVSTTE 192
Db 1127 SSTVSTTE 1134
|||||

RESULT 6
Y585 ARCFU
ID Y585 ARCFU STANDARD; PRT; 90 AA.
AC O29670;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF0585.
GN AF0585.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,


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RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
DR EMBL; AE001064; AAB90659.1; --
DR PIR; A69323; A69323.
DR TIGR; AF0585; --
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 5 27 POTENTIAL.
FT TRANSMEM 40 62 POTENTIAL.
FT TRANSMEM 67 89 POTENTIAL.
SQ SEQUENCE 90 AA; 10081 MW; CSD18CF7C03B4226 CRC64;

Query Match 3.4%; Score 7; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 VVVVAIL 160
Db 69 VVVVAIL 75

RESULT 7
MAL7 HUMAN STANDARD; PRT; 114 AA.
AC Q13113; Q96E11;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 17 kDa membrane associated protein (D096 protein).
GN MAP17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99034932; PubMed=9815914;
RA Kocher O., Cheresch P., Brown L.F., Lee S.W.;
RT "Identification of a novel gene, selectively up-regulated in human
RT carcinomas, using the differential display technique."
RL Clin. Cancer Res. 1:1209-1215(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Grafham D.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RX CHARACTERIZATION.
RX MEDLINE=96312852; PubMed=8701988;
RA Kocher O., Cheresch P., Lee S.W.;
RT "Identification and partial characterization of a novel membrane-
RT associated protein (MAP17) up-regulated in human carcinomas and
RT modulating cell replication and tumor growth."
RL Am. J. Pathol. 149:493-500(1996).
CC -!- FUNCTION: May play an important role in tumor biology.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- TISSUE SPECIFICITY: Expressed at significant levels only in a
CC single epithelial cell population, the proximal tubular epithelial
CC cells of the kidney. Diffusely expressed in various carcinomas
CC originating from kidney, colon, lung and breast.
CC -----
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CC -----
DR EMBL; U21049; AAA92690.1; --
DR EMBL; AL135960; CAB72104.1; --
DR EMBL; BC012303; AAI12303.1; --
DR MIM; 607178; --
KW Transmembrane.
FT TRANSMEM 33 50 POTENTIAL.
FT CONFLICT 13 13 T -> M (IN REF. 3).
FT CONFLICT 51 51 N -> K (IN REF. 3).
SQ SEQUENCE 114 AA; 12227 MW; 7DEB64C3AF78CB18 CRC64;

Query Match 3.4%; Score 7; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 AVAVFLV 150
Db 36 AVAVFLV 42

RESULT 8
RZPR_ECOLI STANDARD; PRT; 147 AA.
AC P77551;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative RZ endopeptidase from lambdaoid prophage Rac (EC 3.4.-.-)
DE (Fragment).
DE RZPR OR B1362.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
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RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RL "The complete genome sequence of Escherichia coli K-12."
RN Science 277:1453-1474(1997).
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aliba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampa G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map."
RL DNA Res. 3:363-377(1996).
CC -!- FUNCTION: Necessary for host cell lysis. It is believed to code
CC for an endopeptidase that cleaves the amino-carboxyl cross-link
CC between the diaminopimelic acid and D-alanine residues in the
CC murein component of the bacterial cell wall (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY U8. STRONG, TO LAMBDOID
CC PHAGES ENDOPEPTIDASES.
CC -----
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CC -----
CC EMBL; AE000233; AAC74444.1; ALT_INIT.
DR EMBL; D90774; BAAL4959.1; ALT_INIT.
DR EcoGene; EG13366; rzpr.
DR InterPro; IPR004929; Phage lysis.
DR Pfam; PF03245; Phage_lysis; 1.
KW Hypothetical protein; Hydrolase; Protease; Bacteriolytic enzyme;
FT NON TER 1
SQ SEQUENCE 147 AA; 16486 MW; 2F4E85F6663A7692 CRC64;

Query Match 3.4%; Score 7; DB 1; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 LVICIVV 155
DB 4 LVICIVV 10
|||||

RESULT 9
APL_LACLC STANDARD; PRT; 242 AA.
AC Q48630;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alkaline phosphatase like protein.
GN APL.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG1363;
RA Venema K., Haandrikman A., Leenhouts K., Kok J., Venema G.;
RT "Cloning and sequencing of a gene (apl) from Lactococcus lactis that
RT can complement a phoA mutation in Escherichia coli."
RL Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.

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CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the Deda family.
CC -----
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CC -----
CC EMBL; Z29065; CAA82306.1; -.
DR PIR; S39339; S39339.
DR InterPro; IPR000252; Deda.
DR Pfam; PF00597; Deda; 1.
KW Transmembrane.
FT TRANSMEM 48 68 POTENTIAL.
FT TRANSMEM 141 161 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
SQ SEQUENCE 242 AA; 27134 MW; 650A8B314C44BA55 CRC64;

Query Match 3.4%; Score 7; DB 1; Length 242;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 VVVAIIIG 161
DB 180 VVVAIIIG 186
|||||

RESULT 10
CAHC_HUMAN STANDARD; PRT; 354 AA.
AC Q43570; Q9BWG2;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Carbonic anhydrase XII precursor (EC 4.2.1.1) (Carbonate dehydratase
DE XII) (CA-XII) (Tumor antigen HOM-RCC-3.1.3).
GN CAL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Renal cell carcinoma;
RX MEDLINE=98301622; PubMed=9636197;
RA Tuercil O., Sahin U., Vollmar E., Siemer S., Goettert E., Seitz G.,
RA Parkkila A.-K., Shah G.N., Grubb J.H., Pfreundschuh M., Sly W.S.;
RT "Human carbonic anhydrase XII: cDNA cloning, expression, and
RT chromosomal localization of a carbonic anhydrase gene that is
RT overexpressed in some renal cell cancers."
RL Proc. Natl. Acad. Sci. U.S.A. 95:7608-7613(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=98445416; PubMed=9770531;
RA Ivanov S.V., Kuzmin I., Wei M.-H., Pack S., Geil L., Johnson B.E.,
RA Stanbridge E.J., Lerman M.I.;
RT "Down-regulation of transmembrane carbonic anhydrases in renal cell
RT carcinoma cell lines by wild-type von Hippel-Lindau transgenes."
RL Proc. Natl. Acad. Sci. U.S.A. 95:12596-12601(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Eye, and Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 30-292.
RX MEDLINE=21396545; PubMed=11493685;
RA Whittington D.A., Waheed A., Ulmasov B., Shah G.N., Grubb J.H.,
RA Sly W.S., Christianson D.W.;
RT "Crystal structure of the dimeric extracellular domain of human
RT carbonic anhydrase XII, a bitopic membrane protein overexpressed in
RT certain cancer tumor cells";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9545-9550 (2001).
CC -!- FUNCTION: Reversible hydration of carbon dioxide.
CC -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
CC -!- COFACTOR: Zinc (By similarity).
CC -!- ENZYME REGULATION: Inhibited by acetazolamide.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O43570-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O43570-2; Sequence=VSP_000772;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COLON, KIDNEY, PROSTATE,
CC INTESTINE AND ACTIVATED LYMPHOCYTES. EXPRESSED AT MUCH HIGHER
CC LEVELS IN THE RENAL CELL CANCERS THAN IN SURROUNDING NORMAL KIDNEY
CC TISSUE. MODERATELY EXPRESSED IN PANCREAS, OVARY, AND TESTIS.
CC -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
CC family.

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DR EMBL; AF051882; AAC39789.1; -;
DR EMBL; AF037335; AAC63952.1; -;
DR EMBL; BC000278; AAH00278.1; -;
DR EMBL; BC011691; AAH11691.1; -;
DR EMBL; BC023981; AAH23981.1; -;
DR PDB; 1JDO; 17-AUG-01.
DR PDB; 1JC2; 17-AUG-01.
DR Genew; HGNC:1371; CA12.
DR MIM; 603263; -;
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004089; F:carbonate dehydratase activity; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR InterPro; IPR001148; Euk_Coanhd.
DR Pfam; PF00194; carb_anhydrase; 1.
DR ProDom; PD000865; Euk_Coanhd; 1.
DR PROSITE; PS00162; Euk_CO2_ANHYDRASE; 1.
KW Lyase; Zinc; Transmembrane; Signal; Alternative splicing;
KW 3D-structure.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 354 CARBONIC ANHYDRASE XII.
FT DOMAIN 25 301 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 302 322 POTENTIAL.
FT DOMAIN 323 354 CYTOPLASMIC (POTENTIAL).

FT METAL 119 119 ZINC (CATALYTIC).
FT METAL 121 121 ZINC (CATALYTIC).
FT METAL 145 145 ZINC (CATALYTIC).
FT DISULFID 50 230
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 292 302 Missing (in isoform 2).
FT FTid=VSP_000772.
FT TURN 37 38
FT HELIX 40 42
FT HELIX 43 46
FT HELIX 48 51
FT STRAND 59 60
FT HELIX 62 64
FT STRAND 65 67
FT TURN 69 70
FT STRAND 75 77
FT STRAND 80 80
FT TURN 83 84
FT STRAND 86 91
FT STRAND 96 99
FT TURN 102 103
FT STRAND 105 107
FT STRAND 113 122
FT STRAND 124 124
FT TURN 125 126
FT STRAND 127 127
FT STRAND 134 135
FT TURN 136 137
FT STRAND 138 138
FT STRAND 142 150
FT TURN 151 153
FT HELIX 157 160
FT TURN 161 162
FT TURN 164 165
FT STRAND 167 176
FT HELIX 181 187
FT TURN 188 189
FT HELIX 190 193
FT TURN 196 197
FT STRAND 199 203
FT STRAND 206 206
FT HELIX 207 210
FT TURN 215 216
FT STRAND 218 223
FT TURN 228 229
FT STRAND 234 239
FT STRAND 243 245
FT HELIX 247 255
FT STRAND 258 258
FT TURN 262 263
FT STRAND 269 269
FT STRAND 285 287
SQ SEQUENCE 354 AA; 39451 MW; 9016216BF2CA6C0C CRC64;
Query Match 3.4%; Score 7; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 151 ICIVVV 157
Db 316 ICIVVV 322
RESULT 11
QIN_AVIS3
ID_QIN_AVIS3 STANDARD; PRT; 387 AA.
AC P56260;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transforming protein Qin (Oncogene Qin).

GN V-QIN.
OS Avian sarcoma virus (strain 31) (ASV31).
OX Viruses; Retrovirus; Retroviridae; Avian type C retroviruses.
OX NCBI_TaxID=35270;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93281605; PubMed=8099441;
RA Li J., Vogt P.K.;
RT "The retroviral oncogene qin belongs to the transcription factor
RT family that includes the homeotic gene fork head.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4490-4494(1993).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-QIN
CC POLYPEPTIDE.
CC -!- SIMILARITY: Contains 1 fork-head domain.
CC -----
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CC -----
DR EMBL; L10719; -; NOT_ANNOTATED_CDS.
DR HSSP; Q63245; 2HFH.
DR TRANSFAC; T01832; -.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS00039; FORK_HEAD_3; 1.
KW DNA-binding; Nuclear protein; Oncogene.
FT DOMAIN 42 54 POLY-HIS.
FT DOMAIN 55 58 POLY-PRO.
FT DOMAIN 64 67 POLY-ALA.
FT DOMAIN 101 106 POLY-ALA.
FT DNA_BIND 142 233 FORK-HEAD.
SQ SEQUENCE 387 AA; 42283 MW; FEA902F50FFB42F9 CRC64;

Query Match 3.4%; Score 7; DB 1; Length 387;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 HHHHPPP 181
DB 51 HHHHPPP 57
|||||

RESULT 12
BRNQ_HABIN STANDARD; PRT; 436 AA.
AC P71345;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Branched-chain amino acid transport system carrier protein (Branched-
DE chain amino acid uptake carrier).
GN BRNQ OR H10226.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.P., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Praser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: Component of the transport system for branched-chain
CC amino acids (leucine, isoleucine and valine) which is coupled to a
CC proton motive force (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -!- SIMILARITY: BELONGS TO THE BRAC/BRAZ/BRNQ FAMILY OF TRANSPORTERS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U32709; AAC21896.1; -.
DR PIR; D64056; D64056.
DR TIGR; H10226; -.
DR InterPro; IPR004685; Livcs.
DR Pfam; PF05525; Branch_AA_trans; 1.
DR TIGRFAMs; TIGR00796; Livcs; 1.
KW Amino-acid transport; Transport; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 7 27 POTENTIAL.
FT TRANSMEM 43 63 POTENTIAL.
FT TRANSMEM 76 96 POTENTIAL.
FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 148 168 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
FT TRANSMEM 228 248 POTENTIAL.
FT TRANSMEM 277 297 POTENTIAL.
FT TRANSMEM 314 334 POTENTIAL.
FT TRANSMEM 339 359 POTENTIAL.
FT TRANSMEM 411 431 POTENTIAL.
SQ SEQUENCE 436 AA; 47039 MW; FA37EDF6C2193FDF CRC64;

Query Match 3.4%; Score 7; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 VVVAALG 161
DB 58 VVVAALG 64
|||||

RESULT 13
FXGB_CHICK STANDARD; PRT; 451 AA.
AC Q90964;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Forkhead box protein GIB (Forkhead-related protein FKHL1)
DE (Transcription factor BF-1) (Brain factor 1) (BF1) (CBF-1) (Proto-
DE oncogene C-QIN) (N-62-5) (CEQ 3-1).
GN FOXGIB OR FKHL1 OR QIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95132616; PubMed=7831308;
RA Chang H.W., Li J., Kretschmar D., Vogt P.K.;


```
RT "Avian cellular homolog of the qin oncogene.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:447-451(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Retina;
RX MEDLINE=96338226; PubMed=8757134;
RA Yuasa J., Hirano S., Yamagata M., Noda M.;
RT "Visual projection map specified by topographic expression of
transcription factors in the retina.";
RL Nature 382:632-635(1996).
CC -!- FUNCTION: May determine the nasotemporal axis of the retina, and
consequently specify the topographical projection of the retinal
ganglion-cell axons to the tectum by controlling expression of
their target genes.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- TISSUE SPECIFICITY: Retina and brain.
CC -!- DEVELOPMENTAL STAGE: Can be detected in regions including
primordial retina and neuroepithelium by embryonic day 2 (E2). At
E3, expressed in the nasal retina and pigment epithelium as well
as in the telencephalon, and at E7 is expressed in retinal
ganglion cells. Levels begin to decline from E4 and almost
disappear by E10.
CC -!- SIMILARITY: Contains 1 fork-head domain.
CC
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or send an email to license@isb-sib.ch).
CC
DR EMBL; L36814; AAA66954.1; -.
DR EMBL; U47275; AAB08466.1; -.
DR PIR; A55909; A55909.
DR HSSP; Q63245; 2HFH.
DR TRANSFAC; T01833; -.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS50039; FORK_HEAD_3; 1.
DR Transcription regulation; DNA-binding; Nuclear protein;
KW Developmental protein; Proto-oncogene.
FT DOMAIN 45 54 POLY-HIS.
FT DOMAIN 55 58 POLY-PRO.
FT DOMAIN 64 67 POLY-ALA.
FT DOMAIN 103 106 POLY-ALA.
FT DNA_BIND 142 233 FORK-HEAD.
SQ SEQUENCE 451 AA; 48856 MW; E9E5B407D2321B50 CRC64;

Query Match 3.4%; Score 7; DB 1; Length 451;
Best Local Similarity 100.0%; Pred.No.15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 HHHHPPP 181
DB 51 HHHHPPP 57

RESULT 14
FXGA_HUMAN STANDARD; PRT; 469 AA.
AC P55316;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Forkhead box protein GlA (Forkhead-related protein FKHL2)
DE (Transcription factor BF-2) (Brain factor 2) (BF2) (HFK2).
GN FOXG1A OR FKHL2.

"Avian cellular homolog of the qin oncogene.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:447-451(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Retina;
RX MEDLINE=96338226; PubMed=8757134;
RA Yuasa J., Hirano S., Yamagata M., Noda M.;
RT "Visual projection map specified by topographic expression of
transcription factors in the retina.";
RL Nature 382:632-635(1996).
CC -!- FUNCTION: May determine the nasotemporal axis of the retina, and
consequently specify the topographical projection of the retinal
ganglion-cell axons to the tectum by controlling expression of
their target genes.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- TISSUE SPECIFICITY: Retina and brain.
CC -!- DEVELOPMENTAL STAGE: Can be detected in regions including
primordial retina and neuroepithelium by embryonic day 2 (E2). At
E3, expressed in the nasal retina and pigment epithelium as well
as in the telencephalon, and at E7 is expressed in retinal
ganglion cells. Levels begin to decline from E4 and almost
disappear by E10.
CC -!- SIMILARITY: Contains 1 fork-head domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
DR EMBL; L36814; AAA66954.1; -.
DR EMBL; U47275; AAB08466.1; -.
DR PIR; A55909; A55909.
DR HSSP; Q63245; 2HFH.
DR TRANSFAC; T01833; -.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS50039; FORK_HEAD_3; 1.
DR Transcription regulation; DNA-binding; Nuclear protein;
KW Developmental protein; Proto-oncogene.
FT DOMAIN 45 54 POLY-HIS.
FT DOMAIN 55 58 POLY-PRO.
FT DOMAIN 64 67 POLY-ALA.
FT DOMAIN 103 106 POLY-ALA.
FT DNA_BIND 142 233 FORK-HEAD.
SQ SEQUENCE 451 AA; 48856 MW; E9E5B407D2321B50 CRC64;

Query Match 3.4%; Score 7; DB 1; Length 451;
Best Local Similarity 100.0%; Pred.No.15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 HHHHPPP 181
DB 51 HHHHPPP 57

RESULT 14
FXGA_HUMAN STANDARD; PRT; 469 AA.
AC P55316;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Forkhead box protein GlA (Forkhead-related protein FKHL2)
DE (Transcription factor BF-2) (Brain factor 2) (BF2) (HFK2).
GN FOXG1A OR FKHL2.

Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95048332; PubMed=7959731;
RA Murphy D.B., Wiese S., Burfeind P., Schmundt D., Mattei M.-G.,
RA Schulz-Schaeffer W., Thies U.;
RT "Human brain factor 1, a new member of the fork head gene family.";
RL Genomics 21:551-557(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95322450; PubMed=7599184;
RA Wiese S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,
RA Schnulle V., Mattei M.-G., Thies U.;
RT "The genes for human brain factor 1 and 2, members of the fork head
gene family, are clustered on chromosome 14q.";
RL Biochim. Biophys. Acta 1262:105-112(1995).
CC -!- FUNCTION: Plays an important role in the establishment of the
regional subdivision of the developing brain and in the
development of the telencephalon. Sequence-specific DNA-binding
protein with a distinct binding specificity (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Contains 1 fork-head domain.
CC
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CC
DR EMBL; X78202; CAA55038.1; -.
DR EMBL; X74143; CAA52240.1; -.
DR PIR; I37451; I37451.
DR HSSP; Q63245; 2HFH.
DR TRANSFAC; T02292; -.
DR Genew; HGNC:3811; FOXG1A.
DR MIM; 600779; -.
DR GO; GO:0003677; F:DNA binding; TAS.
DR GO; GO:0007420; P:brain development; TAS.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS50039; FORK_HEAD_3; 1.
DR Transcription regulation; DNA-binding; Nuclear protein;
KW Developmental protein.
FT DOMAIN 33 56 HIS-RICH.
FT DOMAIN 57 79 PRO-RICH.
FT DOMAIN 70 73 POLY-GLN.
FT DOMAIN 83 88 POLY-ARG.
FT DNA_BIND 161 252 FORK-HEAD.
SQ SEQUENCE 469 AA; 50539 MW; 943B8BDB90008EDC CRC64;

Query Match 3.4%; Score 7; DB 1; Length 469;
Best Local Similarity 100.0%; Pred.No.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 HHHHPPP 181
DB 54 HHHHPPP 60

RESULT 15
FXGB_HUMAN STANDARD; PRT; 477 AA.
ID FXGB_HUMAN
```

AC P55315;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Forkhead box protein GlB (Forkhead-related protein FKHL1)
DE (Transcription factor BF-1) (Brain factor 1) (BFI) (HFK1).
GN FOXG1B OR FKHL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95048332; PubMed=7959731;
RA Murphy D.B., Wiese S., Burfeind P., Schmudt D., Mattei M.-G.,
RA Schulz-Schaeffer W., Thies U.;
RT "Human brain factor 1, a new member of the fork head gene family.";
RL Genomics 21:551-557(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95322450; PubMed=7599184;
RA Wiese S., Murphy D.B., Schlung A., Burfeind P., Schmudt D.,
RA Schnulle V., Mattei M.-G., Thies U.;
RT "The genes for human brain factor 1 and 2, members of the fork head
gene family, are clustered on chromosome 14q.";
RL Biochim. Biophys. Acta 1262:105-112(1995).
CC -!- FUNCTION: Plays an important role in the establishment of the
regional subdivision of the developing brain and in the
development of the telencephalon. Sequence-specific DNA-binding
protein with a distinct binding specificity (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Contains 1 fork-head domain.
CC -----
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CC -----
DR EMBL; X74142; CAA52239.1; -.
DR HSSP; Q63245; 2HFH.
DR TRANSFAC; T02350; -.
DR Genew; HGNC:3812; FOXG1B.
DR MIM; 164874; -.
DR GO; GO:0003677; F:DNA binding; TAS.
DR GO; GO:0007420; P:brain development; TAS.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS50039; FORK_HEAD_3; 1.
KW Transcription regulation; DNA-binding; Nuclear protein;
KW Developmental protein.
FT DOMAIN 33 57 HIS-RICH.
FT DOMAIN 58 80 PRO-RICH.
FT DOMAIN 72 75 POLY-GLN.
FT DOMAIN 99 102 POLY-LEU.
FT DNA BIND 168 259 FORK-HEAD.
SQ SEQUENCE 477 AA; 51340 MW; 71CFD0BD069CFAD5 CRC64;

Query Match 3.4%; Score 7; DB 1; Length 477;
Best Local Similarity 100.0%; Pred.No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 175 FHHHPPP 181
|||||||

Db 54 HHHHPPP 60
Search completed: April 22, 2004, 10:24:02
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 10:15:30 ; Search time 26 Seconds
(without alignments)
762.133 Million cell updates/sec

Title: US-09-935-390A-23
Perfect score: 206
Sequence: 1 MERRHPVCGTCQPTQFRCS.....TVSTTEDTEHLVYNHTIRPL 206

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_78.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	11	5.3	972	A30363	glycoprotein GP330
2	11	5.3	4660	T42737	gp330 protein prec
3	8	3.9	610	A33650	dopamine beta-mono
4	8	3.9	759	D89946	protein-export mem
5	8	3.9	1241	T37190	nephrin - human
6	8	3.9	1743	T26859	hypothetical prote
7	7	3.4	90	A69323	hypothetical prote
8	7	3.4	116	E48338	hypothetical prote
9	7	3.4	135	G97172	hypothetical prote
10	7	3.4	152	S49230	glycine cleavage s
11	7	3.4	159	T38729	hypothetical prote
12	7	3.4	161	S60198	glycine cleavage s
13	7	3.4	173	A72620	probable NADH dehy
14	7	3.4	202	D87019	cytochrome C oxida
15	7	3.4	217	A13429	transposase BME14
16	7	3.4	221	S20964	ribosomal protein
17	7	3.4	222	T03540	cobalamin biosynth
18	7	3.4	222	H96711	hypothetical prote
19	7	3.4	242	S39339	alkaline phosphata
20	7	3.4	256	H36857	B26R protein - var
21	7	3.4	281	T20743	hypothetical prote
22	7	3.4	283	B69713	required for compl
23	7	3.4	288	T17737	proline-rich prote
24	7	3.4	317	AC0464	cell division prot
25	7	3.4	346	E89836	hypothetical prote
26	7	3.4	368	T36414	probable iron-side
27	7	3.4	387	A47446	HNF-3/fork head fa
28	7	3.4	388	T18937	hypothetical prote
29	7	3.4	394	T20633	hypothetical prote

30	7	3.4	405	2	T21188	hypothetical prote
31	7	3.4	408	2	B81417	hypothetical prote
32	7	3.4	436	2	D64056	branched-chain ami
33	7	3.4	451	2	A55909	transforming prote
34	7	3.4	460	1	S51516	serine-type carbox
35	7	3.4	469	2	I37451	HBFG-2 (HFK-2) pro
36	7	3.4	476	2	A54743	transcription fact
37	7	3.4	480	2	JH0672	brain factor 1 pro
38	7	3.4	481	2	JH0377	p70 S6 kinase (BC
39	7	3.4	512	2	E96024	conserved hypothet
40	7	3.4	525	1	A41687	ribosomal protein
41	7	3.4	525	1	TVRTK6	ribosomal protein
42	7	3.4	525	1	S12906	probable ribosomal
43	7	3.4	527	2	C97170	ucharakterized pro
44	7	3.4	537	2	AB2766	sulfate permease [
45	7	3.4	537	2	F97546	hypothetical prote

ALIGNMENTS

RESULT 1

A30363
glycoprotein GP330, renal - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A30363
R;Raychowdhury, R.; Niles, J.L.; McCluskey, R.T.; Smith, J.A.
Science 244, 1163-1165, 1989
A;Title: Autoimmune target in Heymann nephritis is a glycoprotein with homology to the
A;Reference number: A30363; MUID:89266937; PMID:2786251
A;Accession: A30363
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-972 <RAY>
C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-bindin
C;Keywords: glycoprotein
F;24-63/Domain: EGF homology <EGF>
F;64-98/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;105-140/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;149-183/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;189-223/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;227-262/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;270-306/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;311-345/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;352-388/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F;396-430/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F;435-469/Domain: LDL receptor ligand-binding repeat homology <LDL10>
F;479-515/Domain: LDL receptor ligand-binding repeat homology <LDL11>
F;520-557/Domain: LDL receptor ligand-binding repeat homology <LDL12>
F;565-599/Domain: LDL receptor ligand-binding repeat homology <LDL13>
F;705-747/Domain: LDL receptor YWTD-containing repeat homology <YW1>
F;748-791/Domain: LDL receptor YWTD-containing repeat homology <YW2>
F;793-832/Domain: LDL receptor YWTD-containing repeat homology <YW3>

Query Match 5.3%; Score 11; DB 2; Length 972;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SCTCQPTQFRC 19
Db 186 SCTCQPTQFRC 196

RESULT 2

T42737
gp330 protein precursor - rat
N;Alternate names: megalin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Accession: T42737
R;Saito, A.; Pietromonaco, S.; Loo, A.K.C.; Farquhar, M.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994

A;Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of the gp330 family
A;Reference number: A58173; MUID:95024033; PMID:7937880
A;Accession: T42737
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-4660 <SAI>
A;Cross-references: EMBL:L34049; NID:9561852; PID:9561853; PIDN:AAA51369.1
A;Experimental source: strain Sprague-Dawley; kidney
A;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-4660/Product: gp330 protein #status predicted <NAT>

Query Match 5.3%; Score 11; DB 2; Length 4660;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SGTCPTQFRC 19
|||||
Db 1147 SGTCPTQFRC 1157

RESULT 3
A33650
dopamine beta-monoxygenase (EC 1.14.17.1) precursor, membrane-bound - bovine
N;Alternate names: dopamine beta-hydroxylase
C;Species: Bos primigenius taurus (cattle)
C;Date: 09-Mar-1990 #sequence revision 06-Jan-1995 #text change 05-Nov-1999
C;Accession: A33650; A34925; JH0191; A35279; A41754; A34926; A31802; A12853
R;Taljanidisz, J.; Stewart, L.; Smith, A.J.; Klinman, J.P.
Biochemistry 28, 10054-10061, 1989
A;Title: Structure of bovine adrenal dopamine beta-monoxygenase, as deduced from cDNA and peptide.
A;Reference number: A33650; MUID:90148928; PMID:2620060
A;Accession: A33650
A;Molecule type: mRNA
A;Residues: 1-191, 'C', 193-266, 'RDH', 270-587, 'Q', 588-610 <TAL>
A;Cross-references: GB:J02890
R;Lewis, E.J.; Allison, S.; Fader, D.; Claflin, V.; Baizer, L.
J. Biol. Chem. 265, 1021-1028, 1990
A;Title: Bovine dopamine beta-hydroxylase cDNA. Complete coding sequence and expression
A;Reference number: A34925; MUID:90110081; PMID:1688549
A;Accession: A34925
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 14-610 <LE2>
A;Cross-references: GB:J05160; NID:J162962; PIDN:AAA30490.1; PID:gl62963
R;Wu, H.J.; Farmer, R.J.; Koop, A.H.; Rozansky, D.J.; O'Connor, D.T.
J. Neurochem. 55, 97-105, 1990
A;Title: Molecular cloning, structure, and expression of dopamine-beta-hydroxylase from sheep.
A;Reference number: JH0191; MUID:90285664; PMID:1693949
A;Accession: JH0191
A;Molecule type: mRNA
A;Residues: 14-39, 'S', 41-103, 'D', 105-565, 'LE', 568-610 <WUH>
A;Note: the authors translated the codon UCC for residue 40 as Phe and AAG for residue 20 as Arg.
R;Wang, N.; Southan, C.; Dewolf Jr., W.B.; Wells, T.N.C.; Kruse, L.I.; Leatherbarrow, R.
Biochemistry 29, 6466-6474, 1990
A;Title: Bovine dopamine beta-hydroxylase, primary structure determined by cDNA cloning
A;Reference number: A35279; MUID:91003542; PMID:2207088
A;Accession: A35279
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 33-348, 'R', 350-610 <WAN>
A;Cross-references: GB:J02909
A;Note: the translation shown in Fig. 4 differs from that in Fig. 3 in having 64-Tyr and 64-Leu.
R;Lewis, E.J.; Asnani, L.P.
J. Biol. Chem. 267, 494-500, 1992
A;Title: Soluble and membrane-bound forms of dopamine beta-hydroxylase are encoded by the same gene.
A;Reference number: A41754; MUID:92112699; PMID:1730612
A;Accession: A41754
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-76 <LEW>
R;Robertson, J.G.; Desai, P.R.; Kumar, A.; Farrington, G.K.; Fitzpatrick, P.F.; Villafranca, J.C.

J. Biol. Chem. 265, 1029-1035, 1990
A;Title: Primary amino acid sequence of bovine dopamine beta-hydroxylase.
A;Reference number: A34926; MUID:90110082; PMID:2295597
A;Accession: A34926
A;Status: preliminary
A;Molecule type: protein
A;Residues: 33-55, 'RVV', 59-63, '73', 'F', 75-411, 420-441, 445-465, 468-559, 'C', 561-563, 566-605
R;Taylor, C.S.; Kent, U.M.; Fleming, P.J.
J. Biol. Chem. 264, 14-16, 1989
A;Title: The membrane-binding segment of dopamine beta-hydroxylase is not an uncleaved
A;Reference number: A31802; MUID:89079641; PMID:2909511
A;Accession: A31802
A;Molecule type: protein
A;Residues: 33-37 <TAY>
R;Skotland, T.; Ljones, T.; Flatmark, T.; Sletten, K.
Biochem. Biophys. Res. Commun. 74, 1483-1489, 1977
A;Title: NH-2-terminal sequence of dopamine beta-hydroxylase from bovine adrenal medulla
A;Reference number: A12853; MUID:77134133; PMID:843373
A;Accession: A12853
A;Molecule type: protein
A;Residues: 33-34, 'T', 36-44, 'X', 46-47, 'TX', 50 <SKO>
A;Experimental source: adrenal medulla
A;Note: residue 46 was also sequenced as Ile
R;Robertson, J.G.; Adams, G.W.; Medzihradsky, K.F.; Burlingame, A.L.; Villafranca, J.C.
Biochemistry 33, 11563-11575, 1994
A;Title: Complete assignment of disulfide bonds in bovine dopamine beta-hydroxylase.
A;Reference number: A55893; MUID:95001861; PMID:7918370
A;Contents: annotation; disulfide bonds
C;Comment: Dopamine beta-monoxygenase catalyzes the biosynthetic conversion of dopamine to norepinephrine. Dopamine beta-monoxygenase is a tetrameric glycoprotein bound in both the plasma membrane and the cytosol.
C;Superfamily: peptidylglycine monoxygenase I homology
C;Keywords: catecholamine biosynthesis; copper; glycoprotein; membrane protein; monooxygenase
F;1-610/Product: dopamine beta-monoxygenase, membrane-bound form #status predicted <M>
F;1-32/Domain: signal sequence #link MATS #status predicted <SIG>
F;33-610/Product: dopamine beta-monoxygenase, soluble form #status predicted <MATS>
F;289-512/Domain: peptidylglycine monoxygenase I homology #status predicted
F;57,177,559,604/Binding site: carboxylate (Asn) {covalent} #status predicted
F;147-589,225-276,262-288,383-496,387-558,459-481/Disulfide bonds: #status experimental
F;223/Active site: Tyr #status predicted
F;237,238,255,256/Binding site: copper (His) #status predicted
F;326,328,405,407/Binding site: copper (His) #status predicted
F;339/Binding site: phosphate (Ser) (covalent) #status predicted
F;521,523/Disulfide bonds: interchain #status experimental

Query Match 3.9%; Score 8; DB 2; Length 610;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144 AVAVFLVI 151
|||||
Db 18 AVAVFLVI 25

RESULT 4
D89946
protein-export membrane protein SecDF [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence revision 10-May-2001 #text change 22-Oct-2001
C;Accession: D89946
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogo, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89946
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-759 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701435; PIDN:BA842729.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: secF

Query Match 3.9%; Score 8; DB 2; Length 759;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 IVVVVAIL 160
 |||||
 Db 688 IVVVVAIL 695

RESULT 5
 T37190
 nephrin - human
 C:Species: Homo sapiens (man)
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
 C:Accession: T37190
 R:Kestila, M.; Lenkkeri, U.; Mannikko, M.; Lamerdin, J.; McCready, P.; Putaala, H.; Ruoh-
 ason, K.
 Molecular Cell 1, 575-582, 1998
 A:Title: Positionally cloned Gene for a novel glomerular protein - nephrin - is mutated
 A:Reference number: Z21629; MUID:98325371; PMID:9660941
 A:Accession: T37190
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1241 <KES>
 A:Cross-references: EMBL:AF035835; NID:G3025698; PIDN:AA039687.1; PID:G3025699
 C:Genetics:
 A:Gene: NPHS1
 A:Map position: 19
 A>Note: mutated in congenital nephrotic syndrome of the Finnish type (NPHS1); located in

Query Match 3.9%; Score 8; DB 2; Length 1241;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 SSTVSTTE 192
 |||||
 Db 1127 SSTVSTTE 1134

RESULT 6
 T26859
 hypothetical protein Y43F8B.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T26859
 R:Ainscough, R.
 submitted to the EMBL Data Library, October 1998
 A:Reference number: Z20278
 A:Accession: T26859
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1743 <WIL>
 A:Cross-references: EMBL:AL032623; PIDN:CAA21511.1; CESP:Y43F8B.3
 A:Experimental source: Clone Y43F8B
 C:Genetics:
 A:Gene: CESP:Y43F8B.3
 A:Introns: 65/1; 92/2; 128/1; 229/1; 367/1; 422/1; 486/2; 523/1; 571/1; 628/1; 857/2; 94

Query Match 3.9%; Score 8; DB 2; Length 1743;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 IPRWYYP 88
 |||||
 Db 89 IPRWYYP 96

RESULT 7
 A69323
 hypothetical protein AF0585 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C:Accession: A69323
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsc
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.E
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: A69323
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-90 <KLE>
 A:Cross-references: GB:AE001064; GB:AE000782; NID:G2689387; PIDN:AAB90659.1; PID:G26500

Query Match 3.4%; Score 7; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 VVVVAIL 160
 |||||
 Db 69 VVVVAIL 75

RESULT 8
 E48338
 hypothetical protein orf71 - equine herpesvirus 4 (strain 405/76) (fragment)
 C:Species: equine herpesvirus 4
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 08-Oct-1999
 C:Accession: E48338
 R;Nagesha, H.S.; Crabb, B.S.; Studdert, M.J.
 Arch. Virol. 128, 143-154, 1993
 A:Title: Analysis of the nucleotide sequence of five genes at the left end of the uniq
 A:Reference number: A48338; MUID:93119267; PMID:8380320
 A:Accession: E48338
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-116 <NAG>
 A:Cross-references: GB:M89634; NID:G330929; PIDN:AAA46104.1; PID:G330934
 A>Note: sequence extracted from NCBI backbone (NCBIN:121741, NCBIP:121746)

Query Match 3.4%; Score 7; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 SSTVSTT 191
 |||||
 Db 87 SSTVSTT 93

RESULT 9
 G97172
 hypothetical protein CAC2213 [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: G97172
 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
 .; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: G97172
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-135 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK90170.1; PID:G15025210; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC2213

Query Match 3.4%; Score 7; DB 2; Length 135;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 KQVFGI 129
|||||
Db 32 KQVFGI 38

RESULT 10

S49230
glycine cleavage system protein H precursor (clone HFC2) - Flaveria cronquistii
N;Alternate names: H-protein
C;Species: Flaveria cronquistii
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: S49230; S60197
R;Kopriva, S.; Bauwe, H.
Mol. Gen. Genet. 249, 111-116, 1995
submitted to the EMBL Data Library, September 1994
A;Description: Molecular cloning and comparative analysis of H-protein of glycine decarboxylase
A;Reference number: S49229
A;Accession: S49230
A;Molecule type: DNA
A;Residues: 1-152 <KOP>
A;Cross-references: EMBL:Z37518; NID:G547518; PIDN:CAA85755.1; PID:G547519
R;Kopriva, S.; Bauwe, H.
Mol. Gen. Genet. 249, 111-116, 1995
A;Title: H-protein of glycine decarboxylase is encoded by multigene families in Flaveria
A;Reference number: S60194; MUID:96140454; PMID:8552027
A;Accession: S60197
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 8-148 <KOW>
A;Cross-references: EMBL:Z37518
A;Experimental source: tissue type leaf
C;Genetics:

A;Genome: nuclear
C;Superfamily: glycine cleavage system protein H; lipoyl/biotin-binding homology
C;Keywords: lipoamide
F;1-31/Domain: transit peptide (mitochondrion) #status predicted <SIG>
F;32-152/Product: glycine cleavage system protein H #status predicted <MAT>
F;55-129/Domain: lipoyl/biotin-binding homology <LPB>
F;94/Binding site: lipoamide (lys) (covalent) #status predicted

Query Match 3.4%; Score 7; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 VDLPTDG 75
|||||
Db 72 VDLPTDG 78

RESULT 11

T38729
hypothetical protein SPAC3G6.10c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C;Accession: T38729
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21797
A;Accession: T38729
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-159 <GEN>
A;Cross-references: EMBL:Z99167; PIDN:CAB16286.1; GSPDB:GN00066; SPDB:SPAC3G6.10c
A;Experimental source: strain 972h-; cosmid c3G6
C;Genetics:

A;Gene: SPDB:SPAC3G6.10c
A;Map position: 1
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC3G6.10c

Query Match 3.4%; Score 7; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 SSTVSTT 191
|||||
Db 22 SSTVSTT 28

RESULT 12

S60198
glycine cleavage system protein H precursor (clone HFP13) - Flaveria pringlei (fragment)
N;Alternate names: H-protein
C;Species: Flaveria pringlei
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
C;Accession: S60198
R;Kopriva, S.; Bauwe, H.
Mol. Gen. Genet. 249, 111-116, 1995
submitted to the EMBL Data Library, September 1994
A;Title: H-protein of glycine decarboxylase is encoded by multigene families in Flaveria
A;Reference number: S60194; MUID:96140454; PMID:8552027
A;Accession: S60198
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-161 <KOP>
A;Cross-references: EMBL:Z37522; NID:G547499; PIDN:CAA85759.1; PID:G547500
A;Experimental source: tissue type leaf
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1994
C;Genetics:

A;Genome: nuclear
C;Superfamily: glycine cleavage system protein H; lipoyl/biotin-binding homology
C;Keywords: lipoamide
F;1-30/Domain: transit peptide (mitochondrion) (fragment) #status predicted <SIG>
F;31-161/Product: glycine cleavage system protein H #status predicted <MAT>
F;54-128/Domain: lipoyl/biotin-binding homology <LPB>
F;93/Binding site: lipoamide (lys) (covalent) #status predicted

Query Match 3.4%; Score 7; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 VDLPTDG 75
|||||
Db 71 VDLPTDG 77

RESULT 13

A72620
probable NADH dehydrogenase (ubiquinone) chain 6 APE1418 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: A72620
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: A72620
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <KAW>
A;Cross-references: DDBJ:AP000061; NID:G5104821; PIDN:BAA80415.1; PID:dl044201; PID:G5104821
A;Experimental source: strain K1
C;Genetics:

A;Gene: APE1418

Query Match 3.4%; Score 7; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 VAVFLVI 151
|||||
Db 69 VAVFLVI 75

RESULT 14

D87019
cytochrome C oxidase subunit III [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: D87019
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: D87019
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-202 <STO>
A;Cross-references: GB:AL450380; NID:g13092955; PIDN:CAC31263.1; GSPDB:GN00147
C;Genetics:
A;Gene: ctasB
C;Superfamily: cytochrome-c oxidase chain III

Query Match 3.4%; Score 7; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 DVFGRLR 131
|||
Db 94 DVFGRLR 100

RESULT 15
AI3429
transposase BMEI1423 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AI3429
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,
; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AI3429
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52604.1; PID:g17983423; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1423
A;Map position: 1

Query Match 3.4%; Score 7; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 EMVAVAVF 148
|||
Db 38 EMVAVAVF 44

Search completed: April 22, 2004, 10:25:49
Job time : 28 secs

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OM protein - protein search, using sw model

Run on: April 22, 2004, 10:23:45 ; Search time 361 Seconds
(without alignments)
157.767 Million cell updates/sec

Title: US-09-935-390A-23
Perfect score: 206
Sequence: 1 MERRHPVCSTCQTPQRC.....TVSTTDETHLVNHTTRPL 206

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1133595 seqs, 276475211 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	206	100.0	206	9 US-09-935-390A-23	Sequence 23, Appl
2	206	100.0	513	9 US-09-765-449-18	Sequence 18, Appl
3	145	70.4	529	9 US-09-742-201-2	Sequence 2, Appli
4	145	70.4	529	12 US-10-081-056-42	Sequence 42, Appl
5	145	70.4	529	12 US-10-245-752-10	Sequence 10, Appl
6	145	70.4	529	12 US-10-245-859-10	Sequence 10, Appl
7	145	70.4	529	12 US-10-211-858-12	Sequence 12, Appl
8	145	70.4	529	12 US-10-305-654-42	Sequence 42, Appl
9	145	70.4	529	14 US-10-245-103-10	Sequence 10, Appl
10	145	70.4	529	14 US-10-245-107-10	Sequence 10, Appl
11	145	70.4	529	14 US-10-245-143-10	Sequence 10, Appl
12	145	70.4	529	14 US-10-245-771-10	Sequence 10, Appl
13	145	70.4	529	14 US-10-245-851-10	Sequence 10, Appl
14	145	70.4	529	14 US-10-245-883-10	Sequence 10, Appl
15	145	70.4	529	14 US-10-237-535-10	Sequence 10, Appl

16	145	70.4	529	14	US-10-238-183-10	Sequence 10, Appl
17	145	70.4	529	14	US-10-238-283-10	Sequence 10, Appl
18	145	70.4	529	14	US-10-238-370-10	Sequence 10, Appl
19	145	70.4	529	14	US-10-245-055-10	Sequence 10, Appl
20	145	70.4	529	14	US-10-245-147-10	Sequence 10, Appl
21	145	70.4	529	14	US-10-245-730-10	Sequence 10, Appl
22	145	70.4	529	14	US-10-245-739-10	Sequence 10, Appl
23	145	70.4	529	14	US-10-246-210-10	Sequence 10, Appl
24	145	70.4	529	14	US-10-239-196-10	Sequence 10, Appl
25	145	70.4	529	14	US-10-243-024-10	Sequence 10, Appl
26	145	70.4	529	14	US-10-243-409-10	Sequence 10, Appl
27	145	70.4	529	14	US-10-245-621-10	Sequence 10, Appl
28	145	70.4	529	14	US-10-245-880-10	Sequence 10, Appl
29	145	70.4	529	14	US-10-245-033-10	Sequence 10, Appl
30	145	70.4	529	14	US-10-243-095-10	Sequence 10, Appl
31	145	70.4	529	14	US-10-245-185-10	Sequence 10, Appl
32	145	70.4	529	14	US-10-245-427-10	Sequence 10, Appl
33	145	70.4	529	14	US-10-245-473-10	Sequence 10, Appl
34	145	70.4	529	14	US-10-245-770-10	Sequence 10, Appl
35	145	70.4	529	14	US-10-245-877-10	Sequence 10, Appl
36	145	70.4	529	14	US-10-246-976-10	Sequence 10, Appl
37	145	70.4	529	14	US-10-243-320-10	Sequence 10, Appl
38	145	70.4	529	14	US-10-242-743-10	Sequence 10, Appl
39	145	70.4	529	14	US-10-242-845-10	Sequence 10, Appl
40	145	70.4	529	14	US-10-223-085-42	Sequence 42, Appl
41	145	70.4	529	14	US-10-237-636-10	Sequence 10, Appl
42	145	70.4	529	14	US-10-239-325-10	Sequence 10, Appl
43	145	70.4	529	14	US-10-238-346-10	Sequence 10, Appl
44	145	70.4	529	14	US-10-238-411-10	Sequence 10, Appl
45	145	70.4	529	14	US-10-243-124-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-935-390A-23
; Sequence 23, Application US/099353390A
; Patent No. US20020076761A1
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
; Quianjin, Hu
; Garcia, Pablo
; Williams, Lewis T.
; Kothakota, Srinivas
; TITLE OF INVENTION: Secreted Human Proteins
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,390A
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/988,671
; FILING DATE: 1997-12-11
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. R. Potter
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 1369.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2718
; TELEFAX: (510) 655-3542

TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20020076761a1e
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-935-390A-23
Query Match 100.0%; Score 206; DB 9; Length 206;
Best Local Similarity 100.0%; Pred. No. 8.5e-196;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
Db 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
QY 61 FPSDKGHCVDLPDTGLCKESIPRWYINPFSEHCAFTYGGCYGNKNFEEQQCLESERG 120
Db 61 FPSDKGHCVDLPDTGLCKESIPRWYINPFSEHCAFTYGGCYGNKNFEEQQCLESERG 120
QY 121 ISKDVFLGLRREIPIPTSGSVEMAVAVFLVICIVVAVAILGYCFFKNQKDFHGHHP 180
Db 121 ISKDVFLGLRREIPIPTSGSVEMAVAVFLVICIVVAVAILGYCFFKNQKDFHGHHP 180
QY 181 PTPASSTVSTTTEDTEHLVYNHTTRPL 206
Db 181 PTPASSTVSTTTEDTEHLVYNHTTRPL 206

RESULT 2
US-09-765-449-18
; Sequence 18, Application US/09765449
; Patent No. US20020098537A1
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; KITAMURA, Naomi
; MIYAZAWA, Keiji
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,449
; FILING DATE: 22-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,558
; FILING DATE: <Unknown>
; INFORMATION FOR SEQ ID NO: 18
; SEQUENCE CHARACTERISTICS:
; LENGTH: 513 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: MKN45
; SEQUENCE DESCRIPTION: SEQ ID NO: 18

US-09-765-449-18
Query Match 100.0%; Score 206; DB 9; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.9e-195;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
Db 308 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 367
QY 61 FPSDKGHCVDLPDTGLCKESIPRWYINPFSEHCAFTYGGCYGNKNFEEQQCLESERG 120
Db 368 FPSDKGHCVDLPDTGLCKESIPRWYINPFSEHCAFTYGGCYGNKNFEEQQCLESERG 427
QY 121 ISKDVFLGLRREIPIPTSGSVEMAVAVFLVICIVVAVAILGYCFFKNQKDFHGHHP 180
Db 428 ISKDVFLGLRREIPIPTSGSVEMAVAVFLVICIVVAVAILGYCFFKNQKDFHGHHP 487
QY 181 PTPASSTVSTTTEDTEHLVYNHTTRPL 206
Db 488 PTPASSTVSTTTEDTEHLVYNHTTRPL 513

RESULT 3
US-09-742-201-2
; Sequence 2, Application US/09742201
; Patent No. US20020123091A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kirchhofer, Daniel K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: for Use in Modulation of Angiogenesis and Cardiovascularization
; FILE REFERENCE: P1861R1US
; CURRENT APPLICATION NUMBER: US/09/742,201
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US00/06884
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 60/253,665
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-201-2

Query Match 70.4%; Score 145; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
Db 324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 383
QY 61 FPSDKGHCVDLPDTGLCKESIPRWYINPFSEHCAFTYGGCYGNKNFEEQQCLESERG 120
Db 384 FPSDKGHCVDLPDTGLCKESIPRWYINPFSEHCAFTYGGCYGNKNFEEQQCLESERG 443
QY 121 ISKDVFLGLRREIPIPTSGSVEMAV 145
Db 444 ISKDVFLGLRREIPIPTSGSVEMAV 468

RESULT 4
US-10-081-056-42
; Sequence 42, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P.Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235PIC1
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/000,000
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 09/664,610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/242,922
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30952
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/747,259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/767,609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/796,498
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US 09/802,706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/808,689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 09/816,744
PRIOR FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: US 09/828,366
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/870,574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17443
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/00000
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 42
LENGTH: 529
TYPE: PRT
ORGANISM: Homosapiens
US-10-081-056-42
Query Match 70.4%; Score 145; DB 12; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERRHPVCSGTCQPTQPRCSNGCCIDSPLECDTTPNCPDASDEAAACEKYTSGFDELQRIH 60
Db 324 MERRHPVCSGTCQPTQPRCSNGCCIDSPLECDTTPNCPDASDEAAACEKYTSGFDELQRIH 383
QY 61 FPSDKXGHCVDLPDTGLCKESIPRWYNNPFSEHCHCARFTYGGCYGNKNFEEEOOCLESRCG 120
Db 384 FPSDKXGHCVDLPDTGLCKESIPRWYNNPFSEHCHCARFTYGGCYGNKNFEEEOOCLESRCG 443
QY 121 ISKDVFLRLRREIPIPISTGSVENAV 145
Db 444 ISKDVFLRLRREIPIPISTGSVENAV 468
RESULT 5
US-10-245-752-10
Sequence 10, Application US/10245752
Publication No. US20030064473A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630RIC66
CURRENT APPLICATION NUMBER: US/10/245,752
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046

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; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 10
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-752-10

Query Match      70.4%; Score 145; DB 12; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNCPCDASDEAAACEKYTSGFDELQRIH 60
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Db      324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNCPCDASDEAAACEKYTSGFDELQRIH 383
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Qy      61 FPSDKGHCVLDLPTGLCKESIPRWYNPFSEHCFARFTYGGCYGNKNFEEQQCLESCRG 120
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Db      384 FPSDKGHCVLDLPTGLCKESIPRWYNPFSEHCFARFTYGGCYGNKNFEEQQCLESCRG 443
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Qy      121 ISKQDVFGRLRREIPIPISTGSVEMAV 145
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Db      444 ISKQDVFGRLRREIPIPISTGSVEMAV 468
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RESULT 6
US-10-245-859-10
; Sequence 10, Application US/10245859
; Publication No. US20030064474A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C78
; CURRENT APPLICATION NUMBER: US/10/245,859
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
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; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 10
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-859-10

Query Match      70.4%; Score 145; DB 12; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNCPCDASDEAAACEKYTSGFDELQRIH 60
      |||
Db      324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNCPCDASDEAAACEKYTSGFDELQRIH 383
      |||

Qy      61 FPSDKGHCVLDLPTGLCKESIPRWYNPFSEHCFARFTYGGCYGNKNFEEQQCLESCRG 120
      |||
Db      384 FPSDKGHCVLDLPTGLCKESIPRWYNPFSEHCFARFTYGGCYGNKNFEEQQCLESCRG 443
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Qy      121 ISKQDVFGRLRREIPIPISTGSVEMAV 145
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Db      444 ISKQDVFGRLRREIPIPISTGSVEMAV 468
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RESULT 7
US-10-211-858-12
; Sequence 12, Application US/10211858
; Publication No. US20030211096A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/211,858
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 12
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-858-12

Query Match 70.4%; Score 145; DB 12; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNDASDEAAACEKYTSGFDELQRIH 60
Db 324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNDASDEAAACEKYTSGFDELQRIH 383

QY 61 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCAFTYGGCYGNKNPFEEQQCLESRCG 120
Db 384 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCAFTYGGCYGNKNPFEEQQCLESRCG 443

QY 121 ISKQDVFLRLRREIPIPISTGSEMAV 145
Db 444 ISKQDVFLRLRREIPIPISTGSEMAV 468

RESULT 8
US-10-305-654-42
; Sequence 42, Application US/10305654
; Publication No. US20030224984A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, J.
; APPLICANT: Paoni, N. F.
; APPLICANT: Stephan, J-P. F.
; APPLICANT: Watanabe, C.K.
; APPLICANT: Wood, W.I.
; APPLICANT: Williams, P.M.
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235R1C1
; CURRENT APPLICATION NUMBER: US/10/305,654
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 42
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-305-654-42

Query Match 70.4%; Score 145; DB 12; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNDASDEAAACEKYTSGFDELQRIH 60
Db 324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNDASDEAAACEKYTSGFDELQRIH 383

QY 61 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCAFTYGGCYGNKNPFEEQQCLESRCG 120
Db 384 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCAFTYGGCYGNKNPFEEQQCLESRCG 443

QY 121 ISKQDVFLRLRREIPIPISTGSEMAV 145
Db 444 ISKQDVFLRLRREIPIPISTGSEMAV 468

RESULT 9
US-10-245-103-10
; Sequence 10, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C112
; CURRENT APPLICATION NUMBER: US/10/245,103
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 10
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-103-10

Query Match 70.4%; Score 145; DB 14; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNDASDEAAACEKYTSGFDELQRIH 60
Db 324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNDASDEAAACEKYTSGFDELQRIH 383

QY 61 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCAFTYGGCYGNKNPFEEQQCLESRCG 120
Db 384 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCAFTYGGCYGNKNPFEEQQCLESRCG 443

QY 121 ISKQDVFLRLRREIPIPISTGSEMAV 145
Db 444 ISKQDVFLRLRREIPIPISTGSEMAV 468

RESULT 10


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US-10-245-107-10
; Sequence 10, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C71
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 10
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-107-10

Query Match      70.4%; Score 145; DB 14; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTTPNCPDASDEAAACEKYTSGFDELQRIH 60
      |||
Db      324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTTPNCPDASDEAAACEKYTSGFDELQRIH 383

QY      61 FPSDKGHCVLDLPTDTGLCKESIPRWYINPFSEHRCARFTYGGCYGNKNPFEEQQCLESRCG 120
      |||
Db      384 FPSDKGHCVLDLPTDTGLCKESIPRWYINPFSEHRCARFTYGGCYGNKNPFEEQQCLESRCG 443

QY      121 ISKQDVFGRLREIPIPISTGSVEMAV 145
      |||
Db      444 ISKQDVFGRLREIPIPISTGSVEMAV 468

RESULT 11
US-10-245-143-10
; Sequence 10, Application US/10245143
; Publication No. US20030068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
```

```
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C90
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 10
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-143-10

Query Match      70.4%; Score 145; DB 14; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTTPNCPDASDEAAACEKYTSGFDELQRIH 60
      |||
Db      324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTTPNCPDASDEAAACEKYTSGFDELQRIH 383

QY      61 FPSDKGHCVLDLPTDTGLCKESIPRWYINPFSEHRCARFTYGGCYGNKNPFEEQQCLESRCG 120
      |||
Db      384 FPSDKGHCVLDLPTDTGLCKESIPRWYINPFSEHRCARFTYGGCYGNKNPFEEQQCLESRCG 443

QY      121 ISKQDVFGRLREIPIPISTGSVEMAV 145
      |||
Db      444 ISKQDVFGRLREIPIPISTGSVEMAV 468

RESULT 12
US-10-245-771-10
; Sequence 10, Application US/10245771
; Publication No. US20030068781A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
```

```
; APPLICANT: Watanbe,Colin
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; APPLICANT: Fong,Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C98
; CURRENT APPLICATION NUMBER: US/10/245,771
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 10
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-771-10

Query Match      70.4%; Score 145; DB 14; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
      |||
Db      324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 383

QY      61 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSHCARFTYGGCYGNKNPFEEQQCLESCRG 120
      |||
Db      384 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSHCARFTYGGCYGNKNPFEEQQCLESCRG 443

QY      121 ISKDVFGRLRREIPIPTSGSVMNAV 145
      |||
Db      444 ISKDVFGRLRREIPIPTSGSVMNAV 468

RESULT 13
US-10-245-851-10
; Sequence 10, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanbe, Colin
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
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; FILE REFERENCE: P3630R1C93
; CURRENT APPLICATION NUMBER: US/10/245,851
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 10
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-851-10

Query Match      70.4%; Score 145; DB 14; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
      |||
Db      324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 383

QY      61 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSHCARFTYGGCYGNKNPFEEQQCLESCRG 120
      |||
Db      384 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSHCARFTYGGCYGNKNPFEEQQCLESCRG 443

QY      121 ISKDVFGRLRREIPIPTSGSVMNAV 145
      |||
Db      444 ISKDVFGRLRREIPIPTSGSVMNAV 468

RESULT 14
US-10-245-883-10
; Sequence 10, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C70
; CURRENT APPLICATION NUMBER: US/10/245,883
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
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; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/177118
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: 60/179851
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 60/180921
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/187202
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/198587
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 60/199614
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/206330
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/206368
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/209832
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/218371
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/222695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/229896
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/230621
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/235147
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/261878
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/261910
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/261939
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; PRIOR APPLICATION NUMBER: 60/262150
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/264395
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/266421
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/267623
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/274399
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/280982
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/282129
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/282199
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; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: 09/267213
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/403297
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/423741
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/802706

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; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 09/872035
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 10/001054
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/081056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 10/119480
; PRIOR FILING DATE: 2002-04-09

Query Match 70.4%; Score 145; DB 14; Length 529;

Best Local Similarity 100.0%; Pred. No. 5.3e-135;

Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MERRHPVCSGTCQPTQPRCSNGCCIDSFLECDTNCPCPDASDEAAACEKYTSGFDELQRIH	60
Db	324	MERRHPVCSGTCQPTQPRCSNGCCIDSFLECDTNCPCPDASDEAAACEKYTSGFDELQRIH	383
Qy	61	FPSDKGHCVLDLPTDTGLCKESIPRWYNNPFSHCARPTTGGCYGNKNFFEEEOQCLESERG	120
Db	384	FPSDKGHCVLDLPTDTGLCKESIPRWYNNPFSHCARPTTGGCYGNKNFFEEEOQCLESERG	443
Qy	121	ISKDVFGRLRREIPIPTSGSVEHAV	145
Db	444	ISKDVFGRLRREIPIPTSGSVEHAV	468

Search completed: April 22, 2004, 10:32:27

Job time : 362 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 08:30:04 ; Search time 70 Seconds
(without alignments)
831.497 Million cell updates/sec

Title: US-09-935-390A-23
Perfect score: 206
Sequence: 1 MERRHPVCSGTCQPTQPRCS.....TVSTTETDEHLVYNHTTRPL 206

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	206	AAW63684	Aaw63684 Human sec
2	206	100.0	348	AAO17713	Aao17713 Human pro
3	206	100.0	348	AAO17718	Aao17718 Human pro
4	206	100.0	513	AAW27368	Aaw27368 Hepatocyt
5	206	100.0	513	AAW92653	Aaw92653 Human HAI
6	157	76.2	487	ABU92043	Abu92043 Human pro
7	145	70.4	529	AAE20113	Aab20113 Human imm
8	145	70.4	529	AAE09332	Aae09332 Human PRO
9	145	70.4	529	AAU86133	Aau86133 Human PRO
10	145	70.4	529	ABB84837	Abb84837 Human PRO
11	145	70.4	529	ABG34034	Abg34034 Human pro
12	145	70.4	529	ABB95443	Abb95443 Human ang
13	145	70.4	529	ADA01278	Ada01278 Human PRO
14	145	70.4	529	ADA43707	Ada43707 Human sec
15	145	70.4	529	ADA43475	Ada43475 Human sec
16	145	70.4	529	ADA01150	Ada01150 Human PRO
17	145	70.4	529	ADA01034	Ada01034 Human sec
18	145	70.4	529	ADA43591	Ada43591 Human sec
19	145	70.4	529	ADA06853	Ada06853 Human PRO
20	145	70.4	529	ADA08341	Ada08341 Novel hum
21	145	70.4	529	ADB99634	Adb99634 Human PRO
22	145	70.4	529	ADB86917	Adb86917 Human PRO
23	145	70.4	529	ADB66072	Adb66072 Human sec
24	145	70.4	529	ADB99750	Adb99750 Human PRO
25	145	70.4	529	ADB99405	Adb99405 Novel hum

26	145	70.4	529	7	ADB65956	Adb65956 Human sec
27	145	70.4	529	7	ADC23354	Adc23354 Human tra
28	145	70.4	529	7	ADC26047	Adc26047 Human PRO
29	145	70.4	529	7	ADD10331	Add10331 Human sec
30	145	70.4	529	7	ADD11291	Add11291 Human sec
31	145	70.4	529	7	ADD37084	Add37084 Human sec
32	145	70.4	529	7	ADB04874	Ade04874 Human PRO
33	145	70.4	529	7	ADE11180	Ade11180 Human PRO
34	145	70.4	529	7	ADD88111	Add88111 Human PRO
35	145	70.4	529	7	ADD95406	Add95406 Human sec
36	145	70.4	529	7	ADE06336	Ade06336 Human PRO
37	145	70.4	529	7	ADE38111	Ade38111 Human PRO
38	145	70.4	529	7	ADD88227	Add88227 Human PRO
39	145	70.4	529	7	ADD90808	Add90808 Human sec
40	145	70.4	529	8	ADE51661	Ade51661 Human sec
41	145	70.4	529	8	ADE51777	Ade51777 Human sec
42	145	70.4	529	8	ADE37635	Ade37635 Human sec
43	145	70.4	529	8	ADE37519	Ade37519 Human sec
44	145	70.4	529	8	ADD95290	Add95290 Human sec
45	145	70.4	529	8	ADE37990	Ade37990 Human PRO

ALIGNMENTS

RESULT 1
AAW63684
ID AAW63684 standard; protein; 206 AA.

XX	AC	AAW63684;			
XX	DT	24-SEP-1998 (first entry)			
XX	DE	Human secreted protein 4.			
XX	KW	Secreted protein; human; cell proliferation; cytokine activity;			
KW	KW	tissue growth; cellular differentiation; regeneration; activin; inhibin;			
KW	KW	chemotactic; haemostatic; thrombolytic; tumour inhibition;			
KW	KW	anti-inflammatory activity; biomarker.			
XX	OS	Homo sapiens.			
XX	PH	Key	Location/Qualifiers		
FT	Domain		68..122		
FT			/note= "kunitz type serine protease inhibitor domain"		
XX	XX	WO9825959-A2.			
XX	PD	18-JUN-1998.			
XX	PF	11-DEC-1997; 97WO-US022787.			
XX	PR	11-DEC-1996; 96US-0032757P.			
XX	PA	(CHIR) CHIRON CORP.			
XX	PI	Escobedo J, Hu Q, Garcia P, Williams LT, Kothakota S;			
XX	DR	WPI; 1998-348453/30.			
XX	DR	N-PSDB; AAV43604.			
PT	PT	Secreted human polypeptides - having cytokine, cell proliferation or			
PT	PT	differentiation, activin or inhibin, tumour inhibition or anti-			
XX	XX	inflammatory activities.			
PS	PS	Claim 1; Page 52; 78pp; English.			
XX	XX	This represents a human secreted protein. The specification provides			
CC	CC	secreted protein sequences (AAW63681 to AAW63699) encoded by the nucleic			
CC	CC	acid sequences shown in AAV43601 to AAV43619. The invention provides a			
CC	CC	method of identifying a secreted polypeptide which is modified by rough			
CC	CC	microsomes. The secreted proteins can be used in assays to determine			
CC	CC	biological activities, such as cytokine, cell proliferation, or cellular			

CC differentiation activities, tissue growth or regeneration, activin or
CC inhibin activity, chemotactic or chemokinetic activity, haemostatic or
CC thrombolytic activity, receptor/ligand activity, tumour inhibition, or
CC anti-inflammatory activity. The proteins can also be used as biomarkers,
CC to identify tissues or cell types which express the proteins, or a stage-
CC or disease-specific alteration in protein expression. They can be used in
CC protein interaction assays, to identify ligands or binding proteins.
CC Compounds which affect the biological activities of the secreted proteins
CC or their ability to interact with specific ligands can be identified
CC using the proteins in screening assays. The proteins and antibodies that
CC bind specifically to the protein can also be used to design diagnostic
CC tests and therapeutic compositions for diseases which may be associated
CC with altered expression of these proteins. Fusion proteins comprising,
CC e.g. signal sequences or transmembrane domains of the proteins can be
CC used to target other protein domains to cellular membrane or they can be
CC secreted extracellularly

SQ Sequence 206 AA;
Query Match 100.0%; Score 206; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.4e-198;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEACEKYTSGFDELQRIH 60
Db 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEACEKYTSGFDELQRIH 60
QY 61 FPSDKGHCVLDLPDTGLCKESIPRWYINPFSEHCARFTYGGCYGNKNPFEEQQCLESRG 120
Db 61 FPSDKGHCVLDLPDTGLCKESIPRWYINPFSEHCARFTYGGCYGNKNPFEEQQCLESRG 120
QY 121 ISKQVFGRLREIPIPTSGSVEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 180
Db 121 ISKQVFGRLREIPIPTSGSVEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 180
QY 181 PTPASSTVSTTEDTEHLVYNHTTRPL 206
Db 181 PTPASSTVSTTEDTEHLVYNHTTRPL 206

RESULT 2
ID AAO17713 standard; protein; 348 AA.
XX AAO17713;
AC AAO17713;
XX 08-AUG-2002 (first entry)
XX Human protease associated protein HPRAP-2.
DE Human; protease associated protein; HPRAP; cancer; inflammation;
XX anti-HIV; antianaemic; antiarteriosclerotic; antiasthmatic; cytostatic;
KW antiinflammatory; hepatotropic; antidiabetic; nephrotropic; antigout;
KW antithyroid; immunosuppressive; thyromimetic; virucide; dermatological;
KW neuroprotective; cardiant; osteopathic; antiarthritic; antiparasitic;
KW antipsoriatic; uropathic; ophthalmological; antirheumatic; tranquiliser;
KW vulnery; antiulcer; immune disorder; gene therapy; HPRAP-2.

OS Homo sapiens.
XX WO9957274-A1.
PN 11-NOV-1999.
XX 28-APR-1999; 99WO-US009190.
XX 01-MAY-1998; 98US-00071709.
PR (INCY-) INCYTE PHARM INC.
XX Hillman JI, Tang YT, Ial P, Corley NC, Guegler KJ, Patterson C;
PI WPI; 2000-062147/05.

DR N-PSDB; AAL46725.
XX Novel human protease associated proteins used for, e.g. the diagnosis and
PT prevention of cell proliferative and immune disorders.
XX Claim 1; Page; 75pp; English.

CC The present invention provides the protein and coding sequences of four
CC human protease associated proteins, designated HPRAP-1, HPRAP-2, HPRAP-3
CC and HPRAP-4. Human protease associated proteins are expressed in cancer
CC and immortalised cell lines and tissues associated with inflammation and
CC the immune response, and so appear to play a role in cell proliferative
CC and immune disorders. The sequences can be used to diagnose, treat or
CC prevent cell proliferative and immune disorders, including actinic
CC keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis,
CC hepatitis, mixed connective tissue disease, myelofibrosis, paroxysmal
CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
CC thrombocythaemia, AIDS, Addison's disease, adult respiratory distress
CC syndrome, allergies, ankylosing spondylitis, amyloidosis, anaemia,
CC asthma, atherosclerosis, autoimmune haemolytic anaemia, autoimmune
CC thyroiditis, bronchitis, cholecystitis, contact dermatitis, Crohn's
CC disease, atopic dermatitis, dermatomyositis, diabetes mellitus,
CC emphysema, episodic lymphopenia with lymphocytotoxicity, erythroblastosis
CC fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis,
CC Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis,
CC hyperesinophilia, irritable bowel syndrome, multiple sclerosis,
CC myasthenia gravis, myocardial or pericardial inflammation,
CC osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
CC Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome,
CC systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis,
CC thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome,
CC infections and trauma. The present sequence is the HPRAP-2 protein. Note:
CC The present sequence is not obtainable from this Derwent basic but was
CC obtained from the Derwent family equivalent US6171790

XX SQ Sequence 348 AA;

Query Match 100.0%; Score 206; DB 3; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.9e-198;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEACEKYTSGFDELQRIH 60
Db 143 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEACEKYTSGFDELQRIH 202
QY 61 FPSDKGHCVLDLPDTGLCKESIPRWYINPFSEHCARFTYGGCYGNKNPFEEQQCLESRG 120
Db 203 FPSDKGHCVLDLPDTGLCKESIPRWYINPFSEHCARFTYGGCYGNKNPFEEQQCLESRG 262
QY 121 ISKQVFGRLREIPIPTSGSVEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 180
Db 263 ISKQVFGRLREIPIPTSGSVEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 322
QY 181 PTPASSTVSTTEDTEHLVYNHTTRPL 206
Db 323 PTPASSTVSTTEDTEHLVYNHTTRPL 348

RESULT 3
ID AAO17718 standard; protein; 348 AA.
XX AAO17718;
AC AAO17718;
XX 08-AUG-2002 (first entry)
XX Human protease associated protein HPRAP-2.

XX Human; protease associated protein; HPRAP; cancer; inflammation;
XX anti-HIV; antianaemic; antiarteriosclerotic; antiasthmatic; cytostatic;
KW antiinflammatory; hepatotropic; antidiabetic; nephrotropic; antigout;
KW antithyroid; immunosuppressive; thyromimetic; virucide; dermatological;
KW neuroprotective; cardiant; osteopathic; antiarthritic; antiparasitic;

KW antipsoriatic; uropathic; ophthalmological; antirheumatic; tranquiliser;
KW vulnerary; antiulcer; immune disorder; gene therapy; HPRAP-2.
XX
OS Homo sapiens.
XX WO9957274-A1.
PN
XX
PD 11-NOV-1999.
XX
XX 28-APR-1999; 99WO-US009190.
PF
XX
XX 01-MAY-1998; 98US-00071709.
PR
XX
XX (INCY-) INCYTE PHARM INC.
PA
XX Hillman JL, Tang YT, Lal P, Corley NC, Guegler KJ, Patterson C;
PI WPI; 2000-062147/05.
XX
XX Novel human protease associated proteins used for, e.g. the diagnosis and
PT prevention of cell proliferative and immune disorders.
PT
XX
XX Disclosure; Page: 75pp; English.
PS
XX The present invention provides the protein and coding sequences of four
CC human protease associated proteins, designated HPRAP-1, HPRAP-2, HPRAP-3
CC and HPRAP-4. Human protease associated proteins are expressed in cancer
CC and immortalised cell lines and tissues associated with inflammation and
CC the immune response, and so appear to play a role in cell proliferative
CC and immune disorders. The sequences can be used to diagnose, treat or
CC prevent cell proliferative and immune disorders, including actinic
CC keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis,
CC hepatitis, mixed connective tissue disease, myelofibrosis, paroxysmal
CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
CC thrombocythaemia, AIDS, Addison's disease, adult respiratory distress
CC syndrome, allergies, ankylosing spondylitis, amyloidosis, anaemia,
CC asthma, atherosclerosis, autoimmune haemolytic anaemia, autoimmune
CC thyroiditis, bronchitis, cholecystitis, contact dermatitis, Crohn's
CC disease, atopic dermatitis, dermatomyositis, diabetes mellitus,
CC emphysema, episodic lymphopenia with lymphocytotoxicity, erythroblastosis
CC fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis,
CC Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis,
CC hypereosinophilia, irritable bowel syndrome, multiple sclerosis,
CC myasthenia gravis, myocardial or pericardial inflammation,
CC osteoarthritis, osteoporosis, pancreatitis, polyomyelitis, psoriasis,
CC Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome,
CC systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis,
CC thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome,
CC infections and trauma. The present sequence is the HPRAP-2 protein, which
CC was used in a homology comparison in the exemplification of the
CC invention. Note: The present sequence was not obtainable from this
CC Derwent basic but was obtained from the Derwent family equivalent
CC US6171790
XX
SQ Sequence 348 AA;

Query Match 100.0%; Score 206; DB 3; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.9e-198;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNCPCDASDEACEKYTSGFDELQRIH 60
DB 143 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNCPCDASDEACEKYTSGFDELQRIH 202
QY 61 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCARFTYGGCYGNKNFEEQQCLESRCG 120
DB 203 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCARFTYGGCYGNKNFEEQQCLESRCG 262
QY 121 ISKQDVFGRLRREIPSTGSGVEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 180
DB 263 ISKQDVFGRLRREIPSTGSGVEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 322
QY 181 PTPASSTVSTTDETHLVNHTTRPL 206

DB 323 PTPASSTVSTTDETHLVNHTTRPL 348
RESULT 4
AAW27368
ID AAW27368 standard; protein; 513 AA.
XX
AC AAW27368;
XX 21-NOV-1997 (first entry)
XX Hepatocyte growth factor activator inhibitor.
DE Inhibition; inhibitor; protease; hepatocyte; growth factor; activation;
KW activator; human; cancer; cell line; MKN45; regulation; regulator;
KW antibody; kinetic study; assay standard.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..35
FT /label= sig_peptide
FT Peptide 36..513
FT /label= mat_peptide
XX EP759467-A2.
PN 26-FEB-1997.
XX
PD 23-JUL-1996; 96EP-00111870.
XX
XX 24-JUL-1995; 95JP-00187135.
PR (MITU) MITSUBISHI CHEM CORP.
XX
XX Shimomura T, Kawaguchi T, Kitamura N, Miyazawa K;
PI WPI; 1997-147516/14.
DR N-PSDB; AAT90038.
XX
XX New hepatocyte growth factor activator inhibitor and DNA - regulates
PT hepatocyte growth factor and/or HGF activator in vivo or in vitro, and
PT are used in kinetic studies.
XX
XX Claim 3; Page 28-30; 38pp; English.
PS
XX The present sequence is an inhibitor of the protease activity of
CC hepatocyte growth factor (HGF) activator (HGFA), which has a molecular
CC weight of about 40 kD when determined by SDS-PAGE. The inhibitor, which
CC was isolated from the human cancer cell line MKN45, can be used as an in
CC vivo or in vitro regulatory factor for HGF or HGFA. It can also be used
CC to raise antibodies, useful in kinetic studies of the inhibitor, or as
CC assay standards
XX
SQ Sequence 513 AA;

Query Match 100.0%; Score 206; DB 2; Length 513;
Best Local Similarity 100.0%; Pred. No. 5.4e-198;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNCPCDASDEACEKYTSGFDELQRIH 60
DB 308 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTNPNCPCDASDEACEKYTSGFDELQRIH 367
QY 61 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCARFTYGGCYGNKNFEEQQCLESRCG 120
DB 368 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCARFTYGGCYGNKNFEEQQCLESRCG 427
QY 121 ISKQDVFGRLRREIPSTGSGVEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 180
DB 428 ISKQDVFGRLRREIPSTGSGVEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 487

Qy 181 PTPASSTVSTTTEDTEHLVYNHTTRPL 206
Db 488 PTPASSTVSTTTEDTEHLVYNHTTRPL 513

RESULT 5
AAW92653
ID AAW92653 standard; protein; 513 AA.
XX
AC AAW92653;
XX
DT 30-APR-1999 (first entry)
XX
DE Human HAI-1 protein.

XX Hepatocyte growth factor; HAI-1; HGF inhibiting factor; human; plasmin;
KW treatment; prevention; protease activity; plasma; urokinase; trypsin.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..35
FT /label= signal_peptide
FT Protein 36..513
FT /label= HAI-1

XX JP11035480-A.

XX 09-FEB-1999.

XX 15-JUL-1997; 97JP-00189480.

XX 15-JUL-1997; 97JP-00189480.

XX (MITU) MITSUBISHI CHEM CORP.

XX WPI; 1999-186215/16.

XX N-PSDB; AAX02200.

XX A preventive and/or treating agent for the diseases caused by the
PT exasperation of activity of protease - inhibits protease activity of
PT hepatocyte growth factor (HGF) activator.

XX Claim 7; Page 6-8; 8pp; Japanese.

XX This invention describes a preventive and/or treating agent for the
CC diseases caused by the exasperation of activity of protease of plasma
CC kallikrein, plasmin, urokinase and trypsin. The agent contains a protein,
CC HAI-1 which has the following properties, M.W. of ca. 40,000 to 57,000
CC Dalton by SDS-PAGE and an activity of inhibiting protease activity of
CC hepatocyte growth factor (HGF) activator. The HGF inhibiting activity of
CC the protein is specific. HAI-1 shows a high inhibiting activity on
CC plasmin, trypsin, HGF activator and plasma kallikrein but substantially
CC no inhibiting activity on thrombin. This sequence represents the human
CC HAI-1 protein

XX SQ Sequence 513 AA;

Query Match 100.0%; Score 206; DB 2; Length 513;
Best Local Similarity 100.0%; Pred. No. 5.4e-198;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERHPVCSGTCQPTQFRCSGCCIDSFLECDTTPNCPDASDEACEKYTSQDELQRIH 60
Db 308 MERHPVCSGTCQPTQFRCSGCCIDSFLECDTTPNCPDASDEACEKYTSQDELQRIH 367

Qy 61 FSDKGHCVDLPDGTGLCKESIPRWYINPFSHCARFYGGCYGNKNFEEQOCLESRCG 120
Db 368 FSDKGHCVDLPDGTGLCKESIPRWYINPFSHCARFYGGCYGNKNFEEQOCLESRCG 427

Qy 121 ISKDVFGRLRREIPSTGSEMAVAVFLVICIVVVAILGYCFFKQKDFGHHHP 180
Db 428 ISKDVFGRLRREIPSTGSEMAVAVFLVICIVVVAILGYCFFKQKDFGHHHP 487

Qy 181 PTPASSTVSTTTEDTEHLVYNHTTRPL 206
Db 488 PTPASSTVSTTTEDTEHLVYNHTTRPL 513

RESULT 6
ABU92043

ID ABU92043 standard; protein; 487 AA.

XX AC ABU92043;

XX DT 15-JUL-2003 (first entry)

XX Human protein modification and maintenance molecule-23 (PMM-23).

XX Human; protein modification and maintenance molecule; PMM; cancer;
KW cell proliferation disorder; atherosclerosis; neurological disorder;
KW epilepsy; Huntington's disease; stroke; immune disorder; allergy;
KW inflammatory disorder; AIDS; developmental disorder; hypothyroidism;
KW Cushing's syndrome; gastrointestinal disorder; epithelial disorder;
KW infection; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic;
KW neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnerary;
KW antiinflammatory; thyromimetic.

XX OS Homo sapiens.

XX PN WO2003031939-A2.

XX PD 17-APR-2003.

XX PF 11-OCT-2002; 2002WO-US032850.

XX PR 12-OCT-2001; 2001US-0329689P.

XX PR 25-OCT-2001; 2001US-0335703P.

XX PR 09-NOV-2001; 2001US-0348887P.

XX PR 28-NOV-2001; 2001US-0334145P.

XX PR 06-DEC-2001; 2001US-0337451P.

XX PR 14-DEC-2001; 2001US-0340584P.

XX (INCY-) INCYTE GENOMICS INC.

XX Ramkumar J, Gorvad AE, Baughn MR, Emerling EM, Yang J, Lee SY;

XX Tran UK, Becha SD, Duggan EM, Lee EA, Griffin JA, Li JX;

XX Sprague WM, Hafalia AJA, Chavla NK, Lehr-Mason PM, Kable AE, Yue H;

XX Marquis JP, Yao MG, Richardson TW, Tang TY, Jin P, Chien D;

XX Bhatia U, Burrill JD, Lee S, Blake JJ, Ho A, Zheng W;

XX WPI; 2003-430274/40.

XX N-PSDB; ACA92438.

XX New human protein modification and maintenance molecules (PMM), useful
PT for diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant PMM expression e.g. cancer, atherosclerosis, or
PT infections.

XX PS Claim 1; Page 263-264; 311pp; English.

XX The present invention relates to the isolation of human protein
CC modification and maintenance molecules (PMM), and the polynucleotide
CC sequences encoding them. A total of 40 PMM polypeptides (designated PMM
CC -1 to PMM-40) are disclosed. The sequences of the invention are useful
CC for diagnosing a condition or disease associated with the expression of
CC PMM in a subject, preparing a polyclonal or monoclonal antibody, and
CC generating an expression profile of a sample containing the
CC polynucleotides. The diseases or conditions associated with decreased
CC expression or overexpression of PMM are cell proliferation disorders
CC (e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy,
CC Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS,
CC allergies), developmental disorders (e.g. hypothyroidism, Cushing's
CC syndrome), gastrointestinal or epithelial disorders, and infections. The
CC PMM polypeptides or their fragments are useful in screening compounds
CC for effectiveness as agonists or antagonists of the polypeptides, or in


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CC altering the expression of the target polynucleotide and compounds that
CC specifically bind to, or modulate the activity of the polypeptide.
CC ABU92021-ABU92060 represent the human PMM polypeptides of the invention
XX
SQ Sequence 487 AA;

Query Match          76.2%; Score 157; DB 6; Length 487;
Best Local Similarity 100.0%; Pred. No. 8.3e-149;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TSGFDELQRIHFPSDKGHCVLDLPTDGLCKESIPRWYINPFSEHCARFTYGGCYGNKNFE 109
   |||||
Db 331 TSGFDELQRIHFPSDKGHCVLDLPTDGLCKESIPRWYINPFSEHCARFTYGGCYGNKNFE 390
   |||||

QY 110 EEQQCLESCRGISKDVFLGRREIPPIPTSGSVEMAVAVFLVICIVVVVAILGYCFFXQNR 169
   |||||
Db 391 EEQQCLESCRGISKDVFLGRREIPPIPTSGSVEMAVAVFLVICIVVVVAILGYCFFXQNR 450
   |||||

QY 170 KDFHGHHPPTPASSTVSTTTEDTEHLVYNHTTRPL 206
   |||||
Db 451 KDFHGHHPPTPASSTVSTTTEDTEHLVYNHTTRPL 487

RESULT 7
AAB20113
ID AAB20113 standard; protein; 529 AA.
XX
AC AAB20113;
XX
DT 30-APR-2001 (first entry)
XX
DE Human immunostimulant PRO256.
XX
KW PRO256; UNQ223; human; immune disease; autoimmune disease; antirheumatic;
KW antiarthritic; antiinflammatory; antianaemic; immunosuppressive;
KW antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide;
KW dermatological; antipsoriatic; antiasthmatic; antiallergic;
KW immunostimulant; protease-inhibitor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..35
FT Modified-site /label= Signal_peptide
FT Protein 29..35
FT /note= "N-myristoylation site"
FT Modified-site 36..529
FT /label= Mature_protein
FT Modified-site 43..49
FT /note= "N-myristoylation site"
FT Modified-site 66..70
FT /note= "Asn is N-glycosylated"
FT Modified-site 161..167
FT /note= "N-myristoylation site"
FT Peptide 193..196
FT /note= "cell attachment sequence"
FT Modified-site 212..218
FT /note= "N-myristoylation site"
FT Modified-site 235..239
FT /note= "Asn is N-glycosylated"
FT Peptide 257..300
FT /note= "pancreatic trypsin inhibitor (Kunitz) family
FT protein motif"
FT Modified-site 281..287
FT /note= "N-myristoylation site"
FT Modified-site 282..288
FT /note= "N-myristoylation site"
FT Modified-site 285..291
FT /note= "N-myristoylation site"
FT Modified-site 310..316
FT /note= "N-myristoylation site"
FT Modified-site 313..319
FT /note= "N-myristoylation site"
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FT Peptide 347..366
FT /note= "low density lipoprotein class A domain protein
FT motif"
FT Peptide 398..441
FT /note= "pancreatic trypsin inhibitor (Kunitz) family
FT protein motif"
FT Modified-site 422..428
FT /note= "N-myristoylation site"
FT Modified-site 423..429
FT /note= "N-myristoylation site"
FT Modified-site 426..432
FT /note= "N-myristoylation site"
FT Domain 466..483
FT /note= "transmembrane domain"
FT Modified-site 523..527
FT /note= "Asn is N-glycosylated"
XX
PN WO200105972-A1.
XX
PD 25-JAN-2001.
XX
PF 15-MAR-2000; 2000WO-US006884.
XX
PR 20-JUL-1999; 99US-0144758P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ;
PI Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2001-103149/11.
DR N-PSDB; AAF30055.
XX
PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for
PT diagnosing and treating immune-related disorders, such as multiple
PT sclerosis, rheumatoid arthritis and diabetes.
XX
PS Claim 20; Fig 12; 127pp; English.
XX
CC The present sequence is that of novel human immunomodulator PRO256
CC (UNQ223), as deduced from cDNA (see AAF30055) isolated from a placental
CC tissue library. PRO256 (58 kDa, pI 6.22) shows sequence homology to human
CC bikunin protein, suggesting protease-inhibitor activity. The invention
CC provides polynucleotides (see AAF30050-62) encoding novel human PRO
CC proteins (see AAB20108-20) including PRO256. Claimed compositions
CC comprising these proteins or their agonists are useful for increasing
CC infiltration of inflammatory cells into a tissue of a mammal, stimulating
CC or enhancing an immune response, or increasing the proliferation of T-
CC lymphocytes in a mammal in response to an antigen. Claimed compositions
CC comprising a PRO polypeptide or its antagonist have the opposite effect.
CC A claimed method for treating an immune related disorder, such as a T
CC cell disorder, involves administering a PRO polypeptide, an agonist
CC antibody or an antagonist antibody. The disorder is selected from
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, demyelinated diseases (such as multiple sclerosis), autoimmune
CC chronic active hepatitis, primary biliary cirrhosis, granulomatous
CC hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative
CC colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's
CC disease, (auto)immune-mediated skin diseases (such as bullous skin
CC disease, erythema multiforme and psoriasis), allergic diseases (such as
CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and
CC urticaria), immunologic diseases of the lung and transplantation
CC associated diseases (such as graft rejection and graft-versus-host
CC disease) (all claimed). Claimed methods of diagnosing these disorders
CC comprise detecting the level of expression of the PRO gene. Also claimed
CC are a method of identifying a compound capable of inhibiting the
CC expression or activity of the PRO polypeptide, vectors, host cells,
CC antibodies, and a method of stimulating the proliferation of T
```

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CC lymphocytes using PRO256
XX
SQ Sequence 529 AA;

Query Match      70.4%; Score 145; DB 4; Length 529;
Best Local Similarity 100.0%; Pred.No. 1e-136;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDAACEKYTSGFDELQRIH 60
   |||||
Db 324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDAACEKYTSGFDELQRIH 383

QY 61 FPSDKGHCVDLPDGLCKESIPRWYINPFSEHCAFTYGGCYGNKNFEEQQCLSCRG 120
   |||||
Db 384 FPSDKGHCVDLPDGLCKESIPRWYINPFSEHCAFTYGGCYGNKNFEEQQCLSCRG 443

QY 121 ISKDDVFLRLRREIPSTGSVEMAV 145
   |||||
Db 444 ISKDDVFLRLRREIPSTGSVEMAV 468

RESULT 8
AAE09332
ID AAE09332 standard; protein; 529 AA.
XX
AC AAE09332;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human PRO256 protein.
XX
KW Human; PRO256 protein; cardiovascular; endothelial; angiogenic disorder;
KW cardiac hypertrophy; trauma; cardiac; age-related macular degeneration;
KW gene therapy; angiogenesis; protease activity; hepatocyte growth factor;
KW peripheral vascular disease; hepatic; renal injury; nephrotropic; tumour;
KW restinosis; tranquilizer; vulnery; cytostatic; hepatotropic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..35 /label= Signal_peptide
FT Modified-site 29..35 /note= "N-myristoylation site"
FT Protein 36..529 /note= "Human mature hepatocyte growth factor activator inhibitor_PRO256"
FT Modified-site 43..49 /note= "N-myristoylation site"
FT Modified-site 66..70 /note= "Asn is N-glycosylated"
FT Modified-site 161..167 /note= "N-myristoylation site"
FT Region 193..199 /note= "Cell attachment sequence"
FT Modified-site 212..218 /note= "N-myristoylation site"
FT Modified-site 235..239 /note= "Asn is N-glycosylated"
FT Region 278..298 /note= "Pancreatic trypsin inhibitor family signature"
FT Modified-site 281..287 /note= "N-myristoylation site"
FT Modified-site 282..288 /note= "N-myristoylation site"
FT Modified-site 285..291 /note= "N-myristoylation site"
FT Modified-site 310..316 /note= "N-myristoylation site"
FT Modified-site 313..319 /note= "N-myristoylation site"
FT Region 419..438 /note= "Pancreatic trypsin inhibitor family signature"
FT

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FT Modified-site 422..428 /note= "N-myristoylation site"
FT FT
FT Modified-site 423..429 /note= "N-myristoylation site"
FT FT
FT Modified-site 426..432 /note= "N-myristoylation site"
FT FT
FT Domain 466..483 /label= Transmembrane_domain
FT Modified-site 523..527 /note= "Asn is N-glycosylated"
XX
PN WO200159100-A2.
XX
PD 16-AUG-2001.
XX
PF 19-DEC-2000; 2000WO-US034756.
XX
PR 11-FEB-2000; 2000WO-US003565.
PR 15-MAR-2000; 2000WO-US006884.
PR 28-NOV-2000; 2000US-0253665P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Gurney AL, Kirchhofer DK, Wood WI;
XX
DR WPI; 2001-541567/60.
DR N-PSDB; AAD16721.
XX
FT An isolated polypeptide designated PRO256 useful for treating a
FT cardiovascular, endothelial, or angiogenic disorder.
XX
PS Claim 47; Fig 2; 124pp; English.
XX
CC The present invention relates to PRO256 or its agonist/antagonist may be
CC used to treat a cardiovascular, endothelial, or angiogenic disorder in a
CC mammal, especially a human with cardiac hypertrophy, trauma, a type of
CC tumour or age-related macular degeneration. PRO256 may be administered
CC together with a cardiovascular, endothelial, or angiogenic agent, a
CC chemotherapeutic agent, a growth inhibitory agent, or a cytotoxic agent.
CC PRO256 may also be used to treat the disorders above, preferably through
CC administration via ex vivo gene therapy. PRO256 or its agonist may be
CC used to inhibit endothelial cell growth, angiogenesis or protease
CC activity of a hepatocyte growth factor, whereas an antagonist of PRO256
CC may be used to stimulate endothelial cell growth, angiogenesis or
CC protease activity of a hepatocyte growth factor. Stimulation or
CC inhibition of the protease activity of a hepatocyte growth factor is
CC preferably carried out where a mammal has a cardiovascular, endothelial,
CC or angiogenic disorder selected from peripheral vascular disease, hepatic
CC or renal injury or a restinosis disorder. The present sequence is human
CC hepatocyte growth factor activator inhibitor, PRO256
XX
SQ Sequence 529 AA;

Query Match      70.4%; Score 145; DB 4; Length 529;
Best Local Similarity 100.0%; Pred.No. 1e-136;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDAACEKYTSGFDELQRIH 60
   |||||
Db 324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDAACEKYTSGFDELQRIH 383

QY 61 FPSDKGHCVDLPDGLCKESIPRWYINPFSEHCAFTYGGCYGNKNFEEQQCLSCRG 120
   |||||
Db 384 FPSDKGHCVDLPDGLCKESIPRWYINPFSEHCAFTYGGCYGNKNFEEQQCLSCRG 443

QY 121 ISKDDVFLRLRREIPSTGSVEMAV 145
   |||||
Db 444 ISKDDVFLRLRREIPSTGSVEMAV 468

RESULT 9
AAU86133
ID AAU86133 standard; protein; 529 AA.

```


XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Goddard J, Paoni NF;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Ye W;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-090516/12.
DR N-PSDB; ABL88092.
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX Claim 11; Fig 42; 565pp; English.
PS ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX Sequence 529 AA;

Query Match 70.4%; Score 145; DB 5; Length 529;
Best Local Similarity 100.0%; Pred. No. 1e-136;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTTPNCPDASDEAAACEKYSFGDELQRIH 60
Db 324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTTPNCPDASDEAAACEKYSFGDELQRIH 383
QY 61 FPSDKGHCVLDLPDTGLCKESIPRWYNNPSEHCAFTYGGCYGNKNFEEBQQCLESRCG 120
Db 384 FPSDKGHCVLDLPDTGLCKESIPRWYNNPSEHCAFTYGGCYGNKNFEEBQQCLESRCG 443
QY 121 ISKDVFLGLRRRPIPISTGSVEMAV 145
Db 444 ISKDVFLGLRRRPIPISTGSVEMAV 468

RESULT 11
ABG34034
ID ABG34034 standard; protein; 529 AA.
XX AC ABG34034;
XX 15-JUL-2002 (first entry)
XX Human Pro peptide #5.
XX Human; PRO; secreted protein; transmembrane protein; genetic disorder;
XX tumour; cancer.
XX Homo sapiens.
XX WO200224888-A2.
XX 28-MAR-2002.
XX 29-AUG-2001; 2001WO-US027099.
XX 01-SEP-2000; 2000US-0229896P.
XX 05-SEP-2000; 2000US-0230621P.
XX 22-SEP-2000; 2000US-0235147P.
XX 10-NOV-2000; 2000WO-US030873.

PR 12-JAN-2001; 2001US-0261878P.
PR 16-JAN-2001; 2001US-0261910P.
PR 16-JAN-2001; 2001US-0261939P.
PR 16-JAN-2001; 2001US-0262150P.
PR 25-JAN-2001; 2001US-0264395P.
PR 02-FEB-2001; 2001US-0266421P.
PR 09-FEB-2001; 2001US-0267623P.
PR 28-FEB-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001US-0274399P.
PR 03-APR-2001; 2001US-0280982P.
PR 04-APR-2001; 2001US-0282129P.
PR 04-APR-2001; 2001US-0282199P.
PR 09-MAY-2001; 2001US-0290589P.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX (GETH) GENENTECH INC.
PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
XX Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX WPI; 2002-362426/39.
DR N-PSDB; ABK69965.
XX New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or for
PT genetic analysis of individuals with genetic disorders.
XX Claim 11; Fig 10; 218pp; English.
XX This invention relates to the cDNA and protein sequences of novel
CC secreted and transmembrane polypeptides PRO polypeptides. The invention
CC also comprises a method for producing the proteins of the invention by
CC recombinant means and antibodies specific for the protein of the
CC invention. The antibody may be used for detecting the PRO proteins of the
CC invention and may be used to modify their activity. Polynucleotides may
CC be used as hybridisation probes for a cDNA library to isolate the full-
CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
CC probes for mapping the gene which encodes that PRO and for genetic
CC analysis of individuals with genetic disorders, in assays to identify
CC other proteins or molecules involved in binding reaction, to generate
CC transgenic animals or knock-out animals which in turn are useful in the
CC development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. The PRO polypeptides are
CC useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The sequences may also be used to detect
CC overexpression on PRO polypeptides in cancerous tumours and for screening
CC for differentially expressed genes using microarray technology. The
CC present sequence represents a human PRO protein of the invention
XX Sequence 529 AA;

Query Match 70.4%; Score 145; DB 5; Length 529;
Best Local Similarity 100.0%; Pred. No. 1e-136;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTTPNCPDASDEAAACEKYSFGDELQRIH 60
Db 324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTTPNCPDASDEAAACEKYSFGDELQRIH 383
QY 61 FPSDKGHCVLDLPDTGLCKESIPRWYNNPSEHCAFTYGGCYGNKNFEEBQQCLESRCG 120
Db 384 FPSDKGHCVLDLPDTGLCKESIPRWYNNPSEHCAFTYGGCYGNKNFEEBQQCLESRCG 443
QY 121 ISKDVFLGLRRRPIPISTGSVEMAV 145
Db 444 ISKDVFLGLRRRPIPISTGSVEMAV 468

RESULT 12
ABB95443
ID ABB95443 standard; protein; 529 AA.
XX AC ABB95443;
XX DT 19-JUL-2002 (first entry)
XX DE Human angiogenesis related protein PRO256 SEQ ID NO: 42.
XX KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
XX KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
XX KW antiarteriosclerotic.
OS Homo sapiens.
XX WO200208284-A2.
XX 31-JAN-2002.
XX 09-JUL-2001; 2001WO-US021735.
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220664P.
XX 28-JUL-2000; 2000WO-US020710.
XX 02-AUG-2000; 2000US-0222695P.
XX 17-AUG-2000; 2000US-00643657.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 07-SEP-2000; 2000US-0230978P.
XX 18-SEP-2000; 2000US-00664610.
XX 18-SEP-2000; 2000US-00665350.
XX 24-OCT-2000; 2000US-0242922P.
XX 08-NOV-2000; 2000US-00709238.
XX 08-NOV-2000; 2000WO-US030952.
XX 10-NOV-2000; 2000WO-US030873.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.
XX 22-JAN-2001; 2001US-00767609.
XX 28-FEB-2001; 2001US-00796498.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2001; 2001WO-US006666.
XX 09-MAR-2001; 2001US-00802706.
XX 14-MAR-2001; 2001US-00808689.
XX 22-MAR-2001; 2001US-00816744.
XX 05-APR-2001; 2001US-00828366.
XX 10-MAY-2001; 2001US-00854208.
XX 10-MAY-2001; 2001US-00854280.
XX 25-MAY-2001; 2001US-00866028.
XX 25-MAY-2001; 2001US-00866034.
XX 25-MAY-2001; 2001WO-US017092.
XX 30-MAY-2001; 2001US-00870574.
XX 30-MAY-2001; 2001WO-US017443.
XX 01-JUN-2001; 2001WO-US017800.
XX 20-JUN-2001; 2001WO-US019692.
XX (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N P.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Paoni NP;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Ye W;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-171999/22.
DR N-PSDB; ABL95581.
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 42; 567pp; English.
XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
SQ Sequence 529 AA;
Query Match 70.4%; Score 145; DB 5; Length 529;
Best Local Similarity 100.0%; Pred. NO. 1e-136;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
Db |||||
QY 61 FPSDKGHCVLDLPTDGLCKESIPRWYNNPFSHCARFTYGGCYGNKNPFEEQOCLESRCG 120
Db |||||
QY 384 FPSDKGHCVLDLPTDGLCKESIPRWYNNPFSHCARFTYGGCYGNKNPFEEQOCLESRCG 443
Db |||||
QY 121 ISKDVFLRLRREIPSTGSVEMAV 145
Db |||||
RESULT 13
ADA01278
ID ADA01278 standard; protein; 529 AA.
XX ADA01278;
AC ADA01278;
XX 06-NOV-2003 (first entry)
DT Human PRO polypeptide #5.
XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW microvascular endothelial cell; endothelial cell tube formation;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX Homo sapiens.
OS US2003068779-A1.
XX 10-APR-2003.
XX 16-SEP-2002; 2002US-00245107.
XX 09-MAY-2001; 2001US-0290589P.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.

PA (GETH) GENENTECH INC.
XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2003-625484/59.
DR N-PSDB; ADA01277.
XX
XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
PT stimulating proliferation of human microvascular endothelial cells, and
PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
PT cells.
XX
XX Claim 11; Fig 10; 307pp; English.
PS
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for inducing endothelial cell
CC tube formation and for treating sports-related joint problems, articular
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
CC represents a human PRO polypeptide of the invention.
XX
SQ Sequence 529 AA;

Query Match 70.4%; Score 145; DB 6; Length 529;
Best Local Similarity 100.0%; Pred. No. 1e-136;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQPRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
DB 324 MERRHPVCSGTCQPTQPRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 383

QY 61 FPSDKGHCVLDLPTDGLCKESIPRWYYPFSEHCARFTYGGCYGNKNFEEBQQCLESRG 120
DB 384 FPSDKGHCVLDLPTDGLCKESIPRWYYPFSEHCARFTYGGCYGNKNFEEBQQCLESRG 443

QY 121 ISKDVFGRLRREIPDSTGSVEMAV 145
DB 444 ISKDVFGRLRREIPDSTGSVEMAV 468

RESULT 14
ADA43707
ID ADA43707 standard; protein; 529 AA.
XX
AC ADA43707;
XX
DT 20-NOV-2003 (first entry)
XX
XX Human secreted/transmembrane polypeptide PRO256.
DE
XX Human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.
XX

OS Homo sapiens.
XX US2003064474-A1.
PN
XX 03-APR-2003.
PD
XX 16-SEP-2002; 2002US-00245859.
XX PF
XX 29-AUG-2001; 2001WO-US027099.
XX PR 18-JUL-2002; 2002US-00197942.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
XX WPI; 2003-605867/57.
DR N-PSDB; ADA43706.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 11; Fig 10; 308pp; English.
PS
XX The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 529 AA;

Query Match 70.4%; Score 145; DB 6; Length 529;
Best Local Similarity 100.0%; Pred. No. 1e-136;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQPRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
DB 324 MERRHPVCSGTCQPTQPRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 383

QY 61 FPSDKGHCVLDLPTDGLCKESIPRWYYPFSEHCARFTYGGCYGNKNFEEBQQCLESRG 120
DB 384 FPSDKGHCVLDLPTDGLCKESIPRWYYPFSEHCARFTYGGCYGNKNFEEBQQCLESRG 443

QY 121 ISKDVFGRLRRRPIPISTGSEMAV 145
DB 444 ISKDVFGRLRRRPIPISTGSEMAV 468

RESULT 15
ADA43475
ID ADA43475 standard; protein; 529 AA.
XX
AC ADA43475;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO256.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.
XX
OS Homo sapiens.
XX
PN US2003073196-A1.
XX
PD 17-APR-2003.
XX
PF 18-SEP-2002; 2002US-00246210.
XX
PR 04-APR-2001; 2001US-0282199P.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2003-743814/70.
DR N-PSDB; ADA43474.
XX
PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
PT PRO21383 useful for stimulating the proliferation or differentiation of
PT chondrocyte cells and detecting the presence of a tumor in a mammal.
XX
PS Claim 11; Fig 10; 307pp; English.
XX

CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 529 AA;

Query Match 70.4%; Score 145; DB 6; Length 529;
Best Local Similarity 100.0%; Pred. No. 1e-136;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERRHPVCSGTCQPTQFRCNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
DB 324 MERRHPVCSGTCQPTQFRCNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 383
QY 61 FPSDKGHCVLDLPDTGLCKESIPRWYINPFSEHCARFTYGGCYGNKNFEEQQCLESCRG 120
DB 384 FPSDKGHCVLDLPDTGLCKESIPRWYINPFSEHCARFTYGGCYGNKNFEEQQCLESCRG 443
QY 121 ISKDVFGRLRRRPIPISTGSEMAV 145
DB 444 ISKDVFGRLRRRPIPISTGSEMAV 468

Search completed: April 22, 2004, 10:23:38
Job time : 72 secs

The invention relates to an isolated secreted/transmembrane (PRO) polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the nucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide, an extracellular domain of PRO with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and an oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptide is useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080 and PRO21383 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006 polypeptides are useful for inhibiting the proliferation of human microvascular endothelial cells. PRO polypeptides are useful for detecting the presence of tumour in a mammal, including tumours of lung, colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and PRO34274 polypeptides are useful for inducing endothelial cell tube formation. PRO or the antibody are useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide. The

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OM nucleic - nucleic search, using sw model

Run on: April 22, 2004, 04:41:39 ; Search time 4177 Seconds
(without alignments)
10759.536 Million cell updates/sec

Title: US-09-935-390A-4
Perfect score: 1505
Sequence: 1 GAATTCGGCAGGAGGACAG.....AAAAAAGTCCTGCGGCGC 1505

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
c 1	1099.4	73.0	1201 13	BX334952
c 2	1009.8	67.1	1056 13	BX382616
c 3	961.2	63.9	1073 13	BX360438
c 4	961	63.9	1192 13	BX381856

c 5	953.2	63.3	1164	13	BX378542	BX378542
c 6	952.6	63.3	1026	13	BX344105	BX344105
c 7	938.8	62.1	1201	9	AL542118	AL542118
c 8	935	62.1	974	13	BX340192	BX340192
c 9	912	60.6	1201	13	BX360812	BX360812
c 10	907	60.3	1200	13	BX336601	BX336601
c 11	902	59.9	1138	13	BX338259	BX338259
c 12	898.4	59.7	1068	13	BX335408	BX335408
c 13	898.2	59.7	1201	13	BX336602	BX336602
c 14	894.4	59.4	1201	9	AL579407	AL579407
c 15	886.6	58.9	1201	9	AL573797	AL573797
c 16	882.2	58.6	1148	13	BX360076	BX360076
c 17	876.6	58.2	1137	13	BX359232	BX359232
c 18	875.4	58.2	994	13	BX360989	BX360989
c 19	868.4	57.7	1201	13	BX357835	BX357835
c 20	864.4	57.4	1183	9	AL558524	AL558524
c 21	864.2	57.4	1108	9	AL558523	AL558523
c 22	861.8	57.3	1201	13	BX339611	BX339611
c 23	858.6	57.0	941	9	AL568344	AL568344
c 24	855.6	56.9	1201	13	BX385809	BX385809
c 25	855	56.8	1201	13	BX336936	BX336936
c 26	854.2	56.8	1201	13	BX382069	BX382069
c 27	851.8	56.6	1201	13	BX399630	BX399630
c 28	851.8	56.6	1201	13	BX399955	BX399955
c 29	841	55.9	1081	13	BX339553	BX339553
c 30	839.4	55.8	971	13	BX338182	BX338182
c 31	832	55.3	1193	9	AL568876	AL568876
c 32	825.4	54.8	888	13	BQ687222	BQ687222
c 33	825	54.8	1200	13	BX386012	BX386012
c 34	825	54.8	1201	13	BX359692	BX359692
c 35	824	54.8	1201	13	BX339564	BX339564
c 36	822.4	54.6	1201	13	BX339949	BX339949
c 37	819.2	54.4	1201	9	AL513561	AL513561
c 38	815.2	54.2	1004	13	BX360990	BX360990
c 39	812.2	54.0	1201	13	BX378957	BX378957
c 40	810.6	53.9	1062	13	BX398328	BX398328
c 41	803.8	53.4	962	13	BX399483	BX399483
c 42	787.6	52.3	862	14	CA488310	CA488310
c 43	785	52.2	899	14	CA489864	CA489864
c 44	784.6	52.1	856	13	BX400601	BX400601
c 45	782.6	52.0	811	12	BG679448	BG679448

ALIGNMENTS

RESULT 1
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LOCUS BX334952 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI009YC11 3-PRIME, mRNA sequence.
ACCESSION BX334952
VERSION BX334952.1 GI:30310380
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7854.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI009AB06NP1&cluster=7854.f. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

FEATURES		Faraday Avenue Genoscope sequence ID : CS0DI009AB06NP1.	
source	Location/Qualifiers		
	1. .1201		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
ORIGIN	/clone="CS0DI009YC11"		
	/tissue type="PLACENTA COT 25-NORMALIZED"		
	/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"		
	/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
Query Match		73.0%;	Score 1099.4; DB 13; Length 1201;
Best Local Similarity		97.1%;	Pred. No. 6.8e-176;
Matches 1115; Conservative		12; Mismatches	20; Indels 1; Gaps 1;
QY	267	GACACCCCAACTGCCCCGACGCGCTCCGACGAGGCTGCTGTGTAATAATACACGAGTGGC	326
Db	1166		
QY	327	TTTGACGAGCTCCAGCGCATCCATTTCCCAAGGACAAAGGGCACTGGCTGGACCTGCCA	386
Db	1106		
QY	387	GACACGSACTCTGCAAGGAGGATCCCGCTGTGTAATAACCCCTTCAGCGAACAC	446
Db	1046	GACACGSACTCTGCAAGGAGGATCCCGCTGTGTAATAACCCCTTCAGCGAACAC	987
QY	447	TGCGCCCGCTTTACCTATGTTGTTGTACGGCAACAAAGAACAACTTTGAGGAAGACGAG	506
Db	986		
QY	507	CAGTGCCTCGAGTCTTGTGCGGCATCTCCAAAGAGGATGTTTGGCTGAGCGGGAA	566
Db	926	CAGTGCCTCGAGTCTTGTGCGGCATCTCCAAAGAGGATGTTTGGCTGAGCGGGAA	867
QY	567	ATCCCATTTCCAGCACAGGCTCTGTGGAGATGGCTGTGCGAGTGTTCCTGGTCACTGTC	626
Db	866		
QY	627	ATTGTGGTGGTAGCCATCTTGGGTACTGCTTCTTCAAGAACAGAGAAAGGACTTC	686
Db	807	ATTGTGGTGGTAGCCATCTTGGGTACTGCTTCTTCAAGAACAGAGAAAGGACTTC	748
QY	687	CACGGACACCAACCAACCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAG	746
Db	747	CACGGACACCAACCAACCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAG	688
QY	747	GACACGAGCACTGGTCTATATACCAACCAACCGCGCCCTCTGAGCCTGGGTCTCACCG	806
Db	687		
QY	807	GCTCTACCTGGCCCTGCTTCCCTGCTTGTCCAAAGGACAGGCTGGGCTGGGAAACTTT	866
Db	627	GCTCTACCTGGCCCTGCTTCCCTGCTTGTCCAAAGGACAGGCTGGGCTGGGAAACTTT	568
QY	867	GGAACCACTCTTGGCTGTTTCCAGGCCCCACTGTGCTCCAGAGACCAAGGCTCCAGCC	926
Db	567		
QY	927	CCTCTTGGAGAAGTCTCAGCTAAGCTCAGCTCTCAGAAAGCTCAAGGTTTGGAGGAG	986
Db	507		
QY	987	CAGAAAACCTTTGGGCCAGAAAGTACCAAGTATAGGACCTGCTGCATAGGAGTTTGA	1046
Db	447	CAGAAAASCTTTGGGCCAGAAAGTACCAAGTATAGGACCTGCTGCATAGGAGTTTGA	388
QY	1047	GGAAGTTGGAGTTTGTTCCTCTGTTCAAAGCTGCTGTCCCTACCCCATGGTGTAGG	1106
Db			

Db	387	GGAAGTTGGAGTTTGTTCCTCTCTGTTCAAAGCTGCTGCTCCCTACCCCATGGTGTAGG	328
QY	1107	AAGAGGAGTGGGTGGTGTGTCAGACCCCTGGAGGCCCAACCCCTGCTCCCTCCGAGCTCCTCT	1166
Db	327	AAGAGGAGTGGGTGGTGTGTCAGACCCCTGGAGGCCCAACCCCTGCTCCCTCCGAGCTCCTCT	268
QY	1167	TCCATGCTGTGCGCCCAAGGGCTGGAGGAAGGACTTCCCTGTGTAGTTTGTCTGTAAAG	1226
Db	267	TCCATGCTGTGCGCCCAAGGGCTGGAGGAAGGACTTCCCTGTGTAGTTTGTCTGTAAAG	208
QY	1227	AGTTGCTTTTGTATTATTAATGCTGTGGCATGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGG	1286
Db	207	AGTTGCTTTTGTATTATTAATGCTGTGGCATGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGG	148
QY	1287	TGGCCTCTCTATCT	1346
Db	147	TGGCCTCTCTATCT	88
QY	1347	CCACCCCTGGCTAGACACAGACAGACAGAGCCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1406
Db	87	CCACCCCTGGCTAGACACAGACAGACAGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	28
QY	1407	CACCCCA 1414	
Db	27	CACCCNA 20	
RESULT 2			
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LOCUS			
DEFINITION			
BX382616 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA			
clone CS0DI083YF21 3-PRIME, mRNA sequence.			
ACCESSION			
BX382616			
VERSION			
BX382616.1 GI:30439963			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE			
1 (bases 1 to 1056)			
AUTHORS			
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.			
TITLE			
Full-length cDNA libraries and normalization			
JOURNAL			
Unpublished (2001)			
COMMENT			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
Bp 191 91006 EVRY cedex - France			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
Library was constructed by Life Technologies, a division of			
Invitrogen. This sequence belongs to sequence cluster 7854.f For			
more information about this cluster, see			
http://www.genoscope.cns.fr/			
cgi-bin/cluster.cgi?seq=CS0DI083CC11NP1&cluster=7854.f. Contact :			
Feng Liang Email : fliang@lifetech.com URL :			
http://fulllength.invitrogen.com/ invitrogen Corporation 1600			
Faraday Avenue Genoscope sequence ID : CS0DI083CC11NP1.			
FEATURES		Location/Qualifiers	
source	1. .1056		
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	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="CS0DI083YF21"		
ORIGIN	/tissue type="PLACENTA COT 25-NORMALIZED"		
	/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"		
	/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
Query Match		67.1%;	Score 1009.8; DB 13; Length 1056;
Best Local Similarity		98.0%;	Pred. No. 9.5e-161;
Matches 1035; Conservative		4; Mismatches	15; Indels 2; Gaps 2;


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QY 823 GCTTCCTGCTTGCCAGGCGAGAGGCTGGCTGGGAAACTTTGGAAACAGACTCTTGC 892
Db |
QY 616 GCTTCCTGCTTGCCAGGCGAGAGGCTGGCTGGGAAACTTTGGAAACAGACTCTTGC 557
Db |
QY 883 CTCTTTCCAGGCCCACTGTGCTCAGAGACAGGCTCCAGCCCTCTTGGAGAGTCT 942
Db |
QY 556 CTGTTTCCAGGCCCACTGTGCTCAGAGACAGGCTCCAGCCCTCTTGGAGAGTCT 497
QY 943 CAGCTAAGCTCAGCTCCTGAGAAAGCTCAAGGTTTGGAGGAGCAGAAACCTTTGGG 1002
Db |
QY 496 CAGCTAAGCTCAGCTCCTGAGAAAGCTCAAGGTTTGGAGGAGCAGAAACCTTTGGG 437
QY 1003 CAGAGTACAGACTAGAGACCTGCTGCTCAGAGACAGGCTCCAGCCCTCTTGGAGT 1062
Db |
QY 436 CAGAGTACAGACTAGAGACCTGCTGCTCAGAGAGTCTTGGAGGAGTCTTGGAGT 377
QY 1063 TTTCTCTGTTCAAGCTGCTGCTCCTACCCCATGCTGCTGCTGCTGCTGCTGCTGCT 1122
Db |
QY 376 TTTCTCTGTTCAAGCTGCTGCTCCTACCCCATGCTGCTGCTGCTGCTGCTGCTGCT 317
QY 1123 TGTGAGACCTGGAGGCCCAACCTGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
Db |
QY 316 TGTGAGACCTGGAGGCCCAACCTGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCT 257
QY 1183 AGGCTGGGAGGAGGAGTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1242
Db |
QY 256 AGGCTGGGAGGAGGAGTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 197
QY 1243 TTTAATGCTGTGGCATGGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1302
Db |
QY 196 TTTAATGCTGTGGCATGGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 137
QY 1303 TCTTCTCTTCCCCCAAGATGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1362
Db |
QY 136 TCTTCTCTTCCCCCAAGATGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 77
QY 1363 CAGCAGACAGAGCCAGGAGAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1422
Db |
QY 76 CAGCAGACAGAGCCAGGAGAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19
QY 1423 CAACATCAGAGCCAGCC 1440
Db |
QY 18 CCACATCAGAGCCCGGCS 1
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RESULT 4
BX381856/c
LOCUS
DEFINITION
BX381856 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI070YJ23 3-PRIME, mRNA sequence.
ACCESSION
BX381856
VERSION
BX381856.1 GI:30451010
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1192)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI070CE12NP1&cluster=7854.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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Paraday Avenue Genoscope sequence ID : CS0DI070CE12NP1.
Location/Qualifiers
1. 1192
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI070YJ23"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
FEATURES
source
ORIGIN
Query Match 63.9%; Score 961; DB 13; Length 1192;
Best Local Similarity 93.9%; Pred. No. 1.6e-152;
Matches 1026; Conservative 25; Mismatches 27; Indels 15; Gaps 5;
QY 373 GCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGGATCCCGCGTGGTACTACCAACC 432
Db |
QY 1101 GCSGSKGACVKKACAGACAMAG--AYTKSAAGAGAGGATCCCGCGTGGTATTAACCAACC 1044
QY 433 CTTTCAGGAAACACTGCGCCCGCTTTACCTATGTTGGTGGTGGTGGTGGTGGTGGTGGTGG 492
Db |
QY 1043 CTTTCAGGAAACAYGSCCCCGCTTTACCTATGTTGGTGGTGGTGGTGGTGGTGGTGGTGG 984
QY 493 TTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGCGCATCTCCAAGAGGATGTGTGTTG 552
Db |
QY 983 TTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGCGCATCTCCAAGAGGATGTGTGTTG 924
QY 553 GCCTGAGGCGGGAATCCCAATCCAGCAGCAGGCTCTGTGGAGATGGCTGTCGCAAGTGT 612
Db |
QY 923 GCCTGAGGCGGGAATCCCAATCCCAACACAGGCTCTGTGGAGATAGTGTGCGCAGTGT 864
QY 613 TCCTGGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 672
Db |
QY 863 TCCTGGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 804
QY 673 AGAGAAAGGACTTCCAGCGGACACACACACACACACACACACACACACACACACACACAC 732
Db |
QY 803 AGAGAAAGGACTTCCAGCGGACACACACACACACACACACACACACACACACACACACAC 744
QY 733 TCTCCACTACCGAGGACACCGGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
Db |
QY 743 TCTCCACTACCGAGGACACCGGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 684
QY 792 GCCTGGTCTCAGCGGCTCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850
Db |
QY 683 GCCTGGTCTCAGCGGCTCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 851 GGCTGGGAAAAAATTTGGAAACAGACTCTTGCCTGTTTCCAGGCGGCTGCTGCTGCTGCTGCT 910
Db |
QY 623 GGCTGGGAAAAAATTTGGAAACAGACTCTTGCCTGTTTCCAGGCGGCTGCTGCTGCTGCTGCT 564
QY 911 GACGAGGCTCCAGCGGCTCTTGGAGAGT-----CTCAGCTAAGCTCAGTCT 960
Db |
QY 563 GACGAGGCTCCAGCGGCTCTTGGAGAGTCTCAGCTAAGCTCAGCTAAGCTCAGCTCAGTCT 504
QY 961 GAGAAAGCTCAAAAGGTTTGGAGGAGCAGAAACCTTGGGCGCAGAGTACCAGACTAGA 1020
Db |
QY 503 GAGAAAGCTCAAAAGGTTTGGAGGAGCAGAAACCTTGGGCGCAGAGTACCAGACTAGA 444
QY 1021 TGGACCTGCTCATAGGAGTGTGGAGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGG 1080
Db |
QY 443 TGGACCTGCTCATAGGAGTGTGGAGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGG 384
QY 1081 GCCTGTCCCTACCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db |
QY 383 GCCTGTCCCTACCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 324
QY 1141 CCAACCTGCTCCCGAGCTCTCTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
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RESULT 6

BX344105/c
LOCUS BX344105 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI057YA06 3-PRIME, mRNA sequence.

ACCESSION BX344105
VERSION BX344105.1 GI:30344237
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1026)

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7854.f For

more information about this cluster, see

http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS1A1015ZA04NP1&cluster=7854.f. Contact:

Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/

Faraday Avenue Genoscope sequence ID: CS1A1015ZA04NP1.

FEATURES

source

1. .1026
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI057YA06"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 63.3%; Score 952.6; DB 13; Length 1026;
Best Local Similarity 98.9%; Pred. No. 4.3e-151;
Matches 996; Conservative 4; Mismatches 3; Indels 4; Gaps 4;
430 ACCCTTCAGCGAACACTGCGCCGCTTACCTATGTTGTTGTTACGGCAACAGAAACA 489
1005 ACCCTTCAGCGAACAC-GCSCCGCTTACCTATGTTGTTGTTACGGCAACAGAAACA 948
490 ACTTTGAGGAGAGCAGCAGTGCCTCGAGTCTTGTGCGGCACTCCAGAGGATGTGT 549
947 ACTTTGAGGAGAGCAGCAGTGCCTCGAGTCTTGTGCGGCACTCCAGAGGATGTGT 889
550 TTGGCCTGAGCGGGAAATCCCAATT-CCCAGCACAGGCTCTGTGGAGATGGCTGTGCA 608
888 TTGGCCTGAGCGGGAAATCCCAATTCCCGAGCACAGGCTCTGTGGAGATGGCTGTGCA 829
609 GTGTTCTGCTCATCTGCATGTTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTCAAG 668
828 GTGTTCTGCTCATCTGCATGTTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTCAAG 769
669 AACCAGAGAAAGGACTTCCACGGACACACACACACACACACACACACACACACACAC 728
768 AACCAGAGAAAGGACTTCCACGGACACACACACACACACACACACACACACACACAC 709
729 ACTGTCTCCACTACCGAGGACACCGGACACCTGGTCTATAACACACACACACACAC 788
708 ACTGTCTCCACTACCGAGGACACCGGACACCTGGTCTATAACACACACACACACAC 649
789 TGAGCCTGGTCTACCGGCTCTACCTGGCCCTGCTTCTGCTTGTCCAAAGGAGAGGCC 848
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Db 528 GAGACAGGGCTCCAGCCCTCTTGGAGAACTCTAGCTAAGCTCAGCTCTGAGAAAGC 469
QY 969 TCAAAGGTTTGGAGAGGAGAGAGAAACCCCTTGGGCCAGAACTACAGACTAGATGGACCTG 1028
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QY 1389 GCTGCATTCGCGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1435
Db 48 GCTGCATTCGCGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2

RESULT 7

AL542118

LOCUS

DEFINITION

AL542118 Homo sapiens PLACENTA Homo sapiens linear EST 12-MAY-2003

5-PRIME, mRNA sequence.

AL542118

VERSION

AL542118.2 GI:30546953

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7854.f For

more information about this cluster, see

http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DE008CB03QP1&cluster=7854.f. Contact:

Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/

Faraday Avenue Genoscope sequence ID: CS0DE008CB03QP1.

Location/Qualifiers

1. .1201

SOURCE

[illegible]

RESULT 8					
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LOCUS	BX340192	974 bp	mRNA	linear	EST 02-MAY-2003
DEFINITION	BX340192	Homo sapiens PLACENTA COT 25-NORMALIZED	Homo sapiens	cdna	
		clone CS0DI083YH19	3-PRIME,	mRNA sequence.	

EX340192
GI:30341878
Homo sapiens (human)
Homo sapiens
Chordata; Vertebrata; Euteleostomi;
Craniata; Vertebrata; Hominidae; Homo.
Catarrhini; Hominidae; Homo.
Jessee, J. and Polayes, D.
Li, W.B.; Gruber, C.;

TITLE
JOURNAL
COMMENT

Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
[http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI083CD10NP1&cluster=7854.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI083CD10NP1&cluster=7854.f). Contact :
Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI083CD10NP1.

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FEATURES
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                /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo (dT)
                    primer. Five prime end enriched, double-strand cDNA was
                    digested with Not I and cloned into the Not I and EcoR V
                    sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN	Query Match	62.1%;	Score 935;	DB 13;	Length 974;
	Best Local Similarity 98.7%;		Pred. No. 4.1e-148;		
	Matches 960;	Conservative 3;	Mismatches 8;	Indels 2;	Gaps 2
QY	457	TTACCTATGGTGGTTGTTTACGGCCAA	CAAGAACAAC	TTTGAGGAAGAGCAGCAGTGCCCTCG	516
			:		
DB	972	TTACCTATGGTGGTTGTWN-TGCAAC	CAAGAACAAC	TTTGAGGAAGAGCAGCAGTGCCCTCG	914
QY	517	AGTCTTGTGCGGCGATCTCCAAGAAGGATGTGTTTGGCTTGAGCGGGGAATCCCCATT-			575
DB	913	AGTCTTGTGCTGGCACTCCAAGAAGGATGTGTTTGGCTTGAGCGGGGAATCCCCATTTC			854
QY	576	CCCAGCACAGGCTCTGTGGAGATGGCTGTGCGCAGTGTTCCTGGTGCATCTGCATTGTGGTG			635
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE008YD05"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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Query Match	62.4%;	Score 938.8;	DB 9;	Length 1201;
Best Local Similarity	94.9%;	Pred. No. 8.8e-149;		
Matches 987;	Conservative 7;	Mismatches 34;	Indels 12;	Gaps 2;
QY	463	ATGGTGGTTGTTACGGCAACAAGAACAACTTTGAGGAAGACGACAGTCCTCGAGTCTT	522	
DB	34	AAGCAGGCTGGTACCGGTCCGGAAATCCCGGGATGGAAGACGACAGTCCTCGAGTCTT	93	
QY	523	GTCCGGGATCTCCAAGAAGGATGTGTTGGCCTGAGCGGGGAATCCCCATTCCCAGCA	582	
DB	94	GTCCGGGATCTCCAAGAAGGATGTGTTGGCCTGAGCGGGGAATCCCCATTCCCAGCA	153	
QY	583	CAGGCTCTGTGGAGATGGCTGTGCGAGTCTTCTGTTCTCTGTTCTCATCTGCAATTGTTGGTGGTAG	642	
DB	154	CAGGCTCTGTGGAGATGGCTGTGCGAGTCTTCTGTTCTCTGTTCTCATCTGCAATTGTTGGTGGTAG	213	
QY	643	CCATCTTGGTTACTGCTTCTTCAAGAACACAGAGAAAGGACTTCCACGGACACCCACC	702	
DB	214	CCATCTTGGTTACTGCTTCTTCAAGAACACAGAGAAAGGACTTCCACGGACACCCACC	273	
QY	703	ACCCACACCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGG	762	
DB	274	ACCCACACCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGG	333	
QY	763	CTATAACCAACACACCGCGGCCCTCTGAGCTGGGTCTCACCGGCTCTCACCTGGCCCT	822	
DB	334	CTATAACCAACACACCGCGGCCCTCTGAGCTGGGTCTCACCGGCTCTCACCTGGCCCT	393	
QY	823	GCTTCCTGCTTGGCAAGGCAGAGGCCCTGGGCTGGGAAATACTTTGGAAACAGACTCTTGC	882	
DB	394	GCTTCCTGCTTGGCAAGGCAGAGGCCCTGGGCTGGGAAATACTTTGGAAACAGACTCTTGC	453	
QY	883	CTGTTTTCCAGGCCACTGTGCTCTCAGAGACACAGGGCTCCAGCCCTCTTGAGAACT	940	
DB	454	CTGTTTTCCAGGCCACTGTGCTCTCAGAGACACAGGGCTCCAGCCCTCTTGAGAACT	513	
QY	941	-----CTCAGCTAAGCTCAGTCTCTGAGAAAGCTCAAGGTTTGGAAAGAGCAGAAA	992	
DB	514	CAGCTAAGCTCAGCTAAGCTCAGTCTCTGAGAAAGCTCAAGGTTTGGAAAGAGCAGAAA	573	
QY	993	ACCTTTGGGCCAGAGTACACAGACTAGATGGACCTGCCTGCATAGGAGTTTGGAGGAAGT	1052	
DB	574	ACCTTTGGGCCAGAGTACACAGACTAGATGGACCTGCCTGCATAGGAGTTTGGAGGAAGT	633	
QY	1053	TGGAGTTTGTCTCTGTCTTCAAAGCTGCCTGTCCCTACCCCATGGTGTACGAAGAGG	1112	
DB	634	TGGAGTTTGTCTCTGTCTTCAAAGCTGCCTGTCCCTACCCCATGGTGTACGAAGAGG	693	
QY	1113	AGTGGGGTGGTGCAGACCTGGAGGCCCAACCCCTGTCTCCCTACCCCATGGTGTACGAAGAGG	1172	
DB	694	AGTGGGGTGGTGCAGACCTGGAGGCCCAACCCCTGTCTCCCTACCCCATGGTGTACGAAGAGG	753	
QY	1173	CTGTGCGCCCGAGGGCTGGGAGGAGGACTTCCCTGTGTAGTTGTGCTGTAAGAGTTGC	1232	
DB	754	CTGTGCGCCCGAGGGCTGGGAGGAGGACTTCCCTGTGTAGTTGTGCTGTAAGAGTTGC	813	
QY	1233	TTTTTGTATTTAATGCTGTGCGATGGTGAAGAGGAGGAGGAGGCTGTGTTGGCCT	1292	
DB	814	TTTTTGTATTTAATGCTGTGCGATGGTGAAGAGGAGGAGGAGGCTGTGTTGGCCT	873	

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Db 853 CCCAGCAGAGGCTCTGTGGAGATTGTGTCGCAGTGTCTCTGGTCACTCTGCAATTGTGGT 794
QY 636 GTGGTAGCCATCTTGGTTACTGCTTCTTCAAGAACAGAGAAAGGACTTCCACGGACAC 695
Db 793 GTGGTAGCCATCTTGGTTACTGCTTCTTCAAGAACAGAGAAAGGACTTCCACGGACAC 734
QY 696 CACCACACACACACACACACACACACACACACACACACACACACACACACACACACAC 755
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QY 756 CACCTGGTCTATACACACACACACACACACACACACACACACACACACACACACAC 815
Db 673 CACCTGGTCTATACACACACACACACACACACACACACACACACACACACACACAC 614
QY 816 TGGCCCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 875
Db 613 TGGCCCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 554
QY 876 CTCTTGCCTGTTTCCAGGCCCCACTGTGCTCTCAGACACACACACACACACACACAC 935
Db 553 CTCTTGCCTGTTTCCAGGCCCCACTGTGCTCTCAGACACACACACACACACACACAC 494
QY 936 GAAGTCTCAGCTAAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 995
Db 493 GAAGTCTCAGCTAAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 434
QY 996 CTTCGGCCAGAGTACCAAGTACCAAGTACCAAGTACCAAGTACCAAGTACCAAGTACCA 1055
Db 433 CTTCGGCCAGAGTACCAAGTACCAAGTACCAAGTACCAAGTACCAAGTACCAAGTACCA 374
QY 1056 AGTTTGTGTTTCTCTGTTTCAAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1115
Db 373 AGTTTGTGTTTCTCTGTTTCAAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 314
QY 1116 GGGTGTGTGTCTCAGACCCCTGGAGGCCCCAACCCCTGTCTCTCTCTCTCTCTCTCTCT 1175
Db 313 GGGTGTGTGTCTCAGACCCCTGGAGGCCCCAACCCCTGTCTCTCTCTCTCTCTCTCTCT 254
QY 1176 TGGCCCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1235
Db 253 TGGCCCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 194
QY 1236 TTGTTTATTTAATGCTGTGGCATGGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1295
Db 193 TTGTTTATTTAATGCTGTGGCATGGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 134
QY 1296 TATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1355
Db 133 TATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 74
QY 1356 CTTAGACACAGCAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 1415
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QY 1416 GGTTCCTCAACAT 1428
Db 13 GGTTCCTCAACAT 1
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RESULT 9
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LOCUS BX360812 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1075YN13 3-PRIME, mRNA sequence.
ACCESSION BX360812
VERSION BX360812.1 GI:30366469
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
```

TITLE
JOURNAL
COMMENT

Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1075CG07NP1&cluster=7854.f. Contact :
Peng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1075CG07NP1.

FEATURES
Source

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/clone="CS0D1075YN13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="First strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 60.6%; Score 912; DB 13; Length 1201;
Best Local Similarity 97.1%; Pred. No. 2.9e-144;
Matches 932; Conservative 5; Mismatches 22; Indels 1; Gaps 1;
QY 482 CAAGAACAACTTTGAGGAAGAGCAGAGTGCCTCGAGTCTTGTGCGGCGCATCTCCAAGAA 541
Db 969 CAACAAGAAACTTTGAGGAGRGACAGTGCCTCGAGTCTTGTGCGGCGCATCTCCAAGAA 910
QY 542 GGATGTGTTTGGCTGAGGCGGGAAATCCCATTCACAGCAGGCTCTGTGGAGATGGC 601
Db 909 GGATGTGTTTGSCTGAGGCGGGAAATCCCATTCACAGCAGGCTCTGTGGAGATGGC 850
QY 602 TGTGCGAGTGTCTGTGTCACTGTGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 661
Db 849 TGTGCGAGTGTCTGT 790
QY 662 CTTCAAGAACAGAGAAAGGACTTCCACGGACACCAACCAACCAACCAACCAACCAACCA 721
Db 789 CTTCAAGAACAGAGAAAGGACTTCCACGGACACCAACCAACCAACCAACCAACCAACCA 730
QY 722 CAGTCCACTGTCTCCACTA CCGAGACACGGAGCACCTGTGTCTATAACCAACCAACCG 781
Db 729 CAGTCCACTGTCTCCACTA CCGAGACACGGAGCACCTGTGTCTATAACCAACCAACCG 670
QY 782 GCGCCCTCTGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGTCTCTGTCTGCGAAGGC 841
Db 669 GCGCCCTCTGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGTCTCTGTCTGCGAAGGC 610
QY 842 AGAGGCTTGGGCTGGGAAACCTTTGGAAACAGACTCTTGGCTGTCTTCCAGGCCCACTG 901
Db 609 AGAGGCTTGGGCTGGGAAACCTTTGGAAACAGACTCTTGGCTGTCTTCCAGGCCCACTG 550
QY 902 TGCCTCAGACACAGGCTCCAGCCCTCTTGGAGAACTCTCAGTAAGCTCAGTCTCTG 961
Db 549 TGCCTCAGACACAGGCTCCAGCCCTCTTGGAGAACTCTCAGTAAGCTCAGTCTCTG 490
QY 962 AGAAGCTCAAAGGTTTGGAGGAGCAGAAACCTTGGCCAGAACTACCACTAGAT 1021
Db 489 AGAAGCTCAAAGGTTTGGAGGAGCAGAAACCTTGGCCAGAACTACCACTAGAT 430
QY 1022 GGACCTGCTGCATAGGAGTTTGGAGGAGTTTGGAGTTTGTCTCTGTCTCAAGCTG 1081
Db 429 GGACCTGCTGCATAGGAGTTTGGAGGAGTTTGGAGTTTGTCTCTGTCTCAAGCTG 370
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Db 369 CCTGTCCCTACCCCATGGTGTAGGAAGAGAGAGTGGGGGGGTGTAGACCTGGAGGCC 310
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RESULT 10
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DEFINITION
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clone CS0DI030YE23 3-PRIME, mRNA sequence.

ACCESSION
BX336601
VERSION
BX336601.1 GI:30337530
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Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1200)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)

COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI030AC12NP1&cluster=7854.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI030AC12NP1.

FEATURES
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 60.3%; Score 907; DB 13; Length 1200;
Best Local Similarity 87.0%; Pred. No. 2.1e-143;
Matches 961; Conservative 49; Mismatches 84; Indels 11; Gaps 2;

Qy 319 CGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGAGCAGCAAGGGGACTGCGTGG 378
Db 1105 SCMGGGKTGTTKSMAMMMVVKGKTTTAMGSGTSCVGGCYYYTTTCCCGCMCMVVG 1046

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Qy 379 ACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGTGGTACTACACCCCTTCA 438
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Qy 439 GCGAACACTGCGCCCGCTTACCTATGTTGGTTGTTACGGCAACAGAACTTTGAGG 498
Db 985 GCGGCCCTGKGGCGGYTTCCYHTGTTGTTCTSRCCAAAMWAGAACWATTTGAGG 926
Qy 499 AAGAGCAGCAGTCCCTCGAGTCTGTGCGGCATCTCCAAAGAAAGGATGTTTGGCTGA 558
Db 925 AAGAGCAGCAGTCCCTCGAGTCTGTGCGGCCTCTCCCMGMMGGATGTTTGGCTGM 866
Qy 559 GCGGGGAAATCCCAATTCAGACACAGGCTCTGTGAGATGGCTGTGCGAGTGTTCCTGG 618
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Qy 619 TCATCTGCATTGTGGTGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAGAACAGAGAA 678
Db 805 TCATCTGCATTGTGGTGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAGAACAGAGAA 746
Qy 679 AGGACTTCCACGGACACACACACACACACACACACACACACACACACACACACACAC 738
Db 745 AGRACCTTCCACGGACACACACACACACACACACACACACACACACACACACACACAC 686
Qy 739 CTACCGAGGACACGGAGCACTGTGGTCTATTAACACACACACACACACACACACACAC 798
Db 685 CTACCGAGGACACGGAGCACTGTGGTCTATTAACACACACACACACACACACACACAC 626
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Qy 859 AAAACTTTGGAACACAGACTCTTGCCTGTTTCCAGGCCACACTGTGCTCAGAGACCAGG 918
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Qy 919 CTCCAGCCCTCTTTGGAGAGT-----CTCAGCTAAGCTCAGCTAAGCTCAGCTCAGAAAGC 968
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Qy 969 TCAAAGGTTTGAAGGAGCAGAAACCTTTGGGCCAGAGTACAGACTAGATGGACCTG 1028
Db 445 TCAAAGGTTTGAAGGAGCAGAAACCTTTGGGCCAGAGTACAGACTAGATGGACCTG 386
Qy 1029 CCTGCATAGGAGTTTGGAGGAGTTGGAGTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1088
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Qy 1089 CTACCCCATGGTCTAGGAGGAGTGGGGTGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1148
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Qy 1149 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCCCGAGGCTGGAGGAAGGACTTCCCTGT 1208
Db 265 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCCCGAGGCTGGAGGAAGGACTTCCCTGT 206
Qy 1209 GTAGTTGTGCTGTAAGAGTTGCTTTTGTATTATTTATGCTGTGGCATGGGTGAAGAG 1268
Db 205 GTAGTTGTGCTGTAAGAGTTGCTTTTGTATTATTTATGCTGTGGCATGGGTGAAGAG 146
Qy 1269 GAGGGAAGAGGCTGTTTGGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328
Db 145 GAGGGAAGAGGCTGTTTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 86
Qy 1329 CTCT-GCCCTTGATCAGCCCTTCCCTGGCCTAGACCAGCAGACAGAGCCAGGAGAGCTC 1387
Db 85 ATCTAGCCCTTGATCAGCCCTTCCCTGGCCTAGACCAGCAGACAGAGCCAGGAGAGGCTC 26
Qy 1388 AGCTGCAATTCGAGCCCTCCACCCC 1412
Db 25 AGCTGCAATTCGAGCCCTCCACCCC 1
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RESULT	14
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LOCUS	AL579407 1201 bp mRNA linear EST 01-JUN-2003
DEFINITION	AL579407 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA clone CSDH004YB13 3-PRIME, mRNA sequence.
ACCESSION	AL579407
VERSION	AL579407.2 GI:31317691
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

COMMENT

On Feb 16, 2001 this sequence replaced ai:12944423

SENTOUSCOPE - CENTRE NATIONAL DE SEQUELCAVE
BP 191 91006 EVRY cedex - France

was not normalized. Library was constructed by Life Techno

7854.f For more information about this cluster, see

cgi-bin/cluster.cgi?seq=CS0DH004CA07NP1&cluster=7854.f. Co

<http://fulllength.invitrogen.com/> Invitrogen Corporation

LOCATION/QUALIFIERS
1 1307

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/program= "NOIIO EXPRES"
/mol type= "MRNA"
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/clone="CS0DH004YB13"
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/cell_line="JURKAT CELL LINE"

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/note="Vector: pCMVSPORT_6; 1st strand cDNA was p

double-strand cDNA was digested with Not I and

LIBRARY WAS NOT NOTIFIED.

h

31; Conservative 45; Mismatches 48; Indels 4; Gaps 4

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9 CSSGTRGTACWAAACCCCTYMRSGAACACACKCCCCGCTTTCCTTATGGTG--TTGTGTT

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THE UNIVERSITY OF CHICAGO

[The following section contains faint, illegible markings and symbols.]

[illegible][illegible]

9 TGCAGCTCCACTGTCTCCACTACCGAGGACACCGAGCACTGGTCTATAACCAACAC

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2 CCGGCCCCCTGAGCCCTGGGTCTACCGGCTCTACCTGGCCCTGCTTCTGCTTGC

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[illegible]

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QY 1019 GATGGACCTGCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGGTTTCTCTGTTCAAAG 1078
Db :|||||
432 GATGGAACCTGCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGGTTTCTCTGTTCAAAG 373
QY 1079 CTGCTGTCTCCATCCCATGGTGTCTAGGAAGAGGAGTGGGGTGGTGTCTAGACCTTGGAGG 1138
Db :|||||
372 CTGCTGTCTCCATCCCATGGTGTCTAGGAAGAGGAGTGGGGTGGTGTCTAGACCTTGGAGG 313
QY 1139 CCCCACCTGTCTCCCGAGCTCTCTTCCATGCTGTGCGCCAGGGCTGGGAGGAAGG 1198
Db :|||||
312 CCCCACCTGTCTCCCGAGCTCTCTTCCATGCTGTGCGCCAGGGCTGGGAGGAAGG 253
QY 1199 ACTTCCCTGTGTAGTTGTCTGTAAAGAGTTGCTTTTGTGTTTAAATGCTGTGGCAT 1258
Db :|||||
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QY 1259 GGGTGAAGAGGAGGGAAGAGGCTGTGTTGGCCCTCTCTATCTCTCTCTCTCTCTCCGCCA 1318
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192 GGGTGAARAGGAGGGAAGAGGCTGTGTTGGCCCTCTCTATCTCTCTCTCTCTCTCCGCCA 133
QY 1319 AGATTGAGCTCTGCTGCTTGTATGATCAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1378
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QY 1379 GAGAAGCTCAGCTGCATTTCCGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1438
Db :|||||
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13 CGCCSSA 6
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RESULT 15

AL573797/c

LOCUS AL573797 1201 bp mRNA linear EST 31-MAY-2003
DEFINITION AL573797 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI055YC15 3-PRIME, mRNA sequence.

ACCESSION

AL573797

VERSION

AL573797.2 GI:31295133

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:12933383.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7854.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI055AB08NP1&cluster=7854.f. Contact:

Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Paraday Avenue Genoscope sequence ID: CS0DI055AB08NP1.

FEATURES

Location/Qualifiers

1..1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI055YC15"

/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN	Query Match	58.9%;	Score 886.6;	DB 9;	Length 1201;
	Best Local Similarity	97.2%;	Pred. No. 5.7e-140;		
	Matches 912;	Conservative	8;	Mismatches 16;	Indels 2;
					Gaps 2;
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Db	941	TKCCTCGAGTCTTGTGCGGCATCTCCAAAGAGGATGTGTTGGCCTGAGCGGGAATC	883		
QY	570	CCCATTCACACACAGGCTCTGTGGAGATGGCTGTGCGAGTGTCTCTGTCATCTGCATT	629		
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Db	642	CTCACCTGCGCCCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	583		
QY	870	ACCAGACTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	929		
Db	582	ACCAGACTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	523		
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QY	1350	CCCTGGCTAGACCAAG	1409		
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QY	1410	CCCCAAGGTTCTCAACATCATCAGCCCAAGCCCGCCAC 1447			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2004, 05:09:18 ; Search time 659 Seconds
(without alignments)
10296.637 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
US-09-935-390A-4
; Sequence 4, Application US/09935390A
; Patent No. US20020076761A1
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
; Quianjin, Hu
; Garcia, Pablo
; Williams, Lewis T.
; Kothakota, Srinivas
; TITLE OF INVENTION: Secreted Human Proteins
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,390A
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/988,671
; FILING DATE: 1997-12-11
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. R. Potter
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 1369.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2718

Query Match		97.5%;	Score 1468;	DB 9;	Length 2482;
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RESULT 3

US-10-081-056-41
; Sequence 41, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pacini, Nicholas F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C1
; CURRENT APPLICATION NUMBER: US/10/081,056
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522

Query Match		97.5%;	Score 1468;	DB 9;	Length 2482;
Best Local Similarity		99.3%;	Pred. No. 0;		
Matches 1474;		Conservative	0;	Mismatches	10;
				Indels	0;
				Gaps	0;
Qy	9	CACGAGAGCAGATCTGCAAGAGTTCGTTTATGGAGGCTGCTGGGCAACAAGAACAC	68		
Db	995	CCACGAGCAGATCTGCAAGAGTTCGTTTATGGAGGCTGCTGGGCAACAAGAACAC	1054		
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	369	CACCTGCTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGTGGTACTAC	428		
Db	1355	CACCTGCTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGTGGTACTAC	1414		
	429	AACCCCTTCAGCGAACACTGCGCCCGCTTACCTATGGTGGTGTGTACGGCAACAAGAAC	488		
Db	1415	AACCCCTTCAGCGAACACTGCGCCCGCTTACCTATGGTGGTGTGTATGGCAACAAGAAC	1474		
	489	AACCTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGCACTCTCCAAGAGGATGTG	548		
Db	1475	AACCTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGCACTCTCCAAGAGGATGTG	1534		
	549	TTTGGCCTGAGCGGGGAAATCCCAATTCACGACACAGGCTCTGTGGAGATGGCTGTGCA	608		
Db	1535	TTTGGCCTGAGCGGGGAAATCCCAATTCACGACACAGGCTCTGTGGAGATGGCTGTGCA	1594		
	609	GTGTTCTCTGATCTGCAATGTGGTGGTAGCCATCTTGGGTACTGCTTCTTCAAG	668		
Db	1595	GTGTTCTCTGATCTGCAATGTGGTGGTAGCCATCTTGGGTACTGCTTCTTCAAG	1654		
	669	AACGAGAGAAAGACTTCCACGGACACCAACCAACCAACCAACCAACCAACCAACCAAC	728		
Db	1655	AACGAGAGAAAGACTTCCACGGACACCAACCAACCAACCAACCAACCAACCAACCAAC	1714		
	729	ACTGTCTCCACTACCGAGGACACCGGACCTGCTGTATACCAACCAACCAACCAACCAAC	788		
Db	1715	ACTGTCTCCACTACCGAGGACACCGGACCTGCTGTATACCAACCAACCAACCAACCAAC	1774		
	789	TGAGCCTGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTCTGCTTGGCAAGGAGGCGC	848		
Db	1775	TGAGCCTGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTCTGCTTGGCAAGGAGGCGC	1834		
	849	TGGGCTGGGAAACCTTTGGAACCAAGACTCTTGCCTGTTTCCAGGCGCCACTGTGCCTCA	908		
Db	1835	TGGGCTGGGAAACCTTTGGAACCAAGACTCTTGCCTGTTTCCAGGCGCCACTGTGCCTCA	1894		
	909	GAGACAGGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGCTCAGCTGAGAAAGC	968		
Db	1895	GAGACAGGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGCTCAGCTGAGAAAGC	1954		
	969	TCAAAGGTTTGGAGGAGCAGAAACCCCTTGGGCGCAGAGTACCAGACTAGATGGACCTG	1028		
Db	1955	TCAAAGGTTTGGAGGAGCAGAAACCCCTTGGGCGCAGAGTACCAGACTAGATGGACCTG	2014		
	1029	CCTGCATAGGAGTTTGGAGGAGTGGAGTTTGTCTCTCTGTTTCAAGACTGCCTGTCC	1088		

;; PRIOR FILING DATE: 2000-08-23
;; PRIOR APPLICATION NUMBER: PCT/US00/23328
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: US 60/230,978
;; PRIOR FILING DATE: 2000-09-07
;; PRIOR APPLICATION NUMBER: US 60/000,000
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: US 09/664,610
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: US 09/665,350
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: US 60/242,922
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 09/709,238
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: PCT/US00/30952
;; PRIOR FILING DATE: 2000-11-08
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;; PRIOR FILING DATE: 2000-12-01
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;; PRIOR FILING DATE: 2000-12-20
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;; PRIOR FILING DATE: 2001-04-05
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;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/00000
;; PRIOR FILING DATE: 2001-06-28
;; NUMBER OF SEQ ID NOS: 383
;; SEQ ID NO 41
;; LENGTH: 2482
;; TYPE: DNA
;; ORGANISM: Homosapiens
US-10-081-056-41

Query Match 97.5%; Score 1468; DB 13; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 9 CACGAGGACGATCTGCAAGAGTTTCGTTATGGAGGCTGTGGGCAACAAGAACAC 68

Db 995 CCCACGAGCAGATCTGCAAGAGTTTCGTTATGGAGGCTGTGGGCAACAAGAACAC 1054
QY 69 TACCTTCGGGAAGAAGAGTGCATTTAGCTGTGCGGGTGTGCAAGGTGGCCTTTGAGA 128
Db 1055 TACCTTCGGGAAGAAGAGTGCATTTAGCTGTGCGGGTGTGCAAGGTGGCCTTTGAGA 1114
QY 129 GGCAGCTCTGGGGCTCAGGCGACTTTCCCCAGGGCCCTCCATGGAAAGCGCCATCCA 188
Db 1115 GGCAGCTCTGGGGCTCAGGCGACTTTCCCCAGGGCCCTCCATGGAAAGCGCCATCCA 1174
QY 189 GTGTGCTCTGGGCACCTGTGAGCCACCCAGTTCCCGTGCAGCAATGGCTGCTGCATCGAC 248
Db 1175 GTGTGCTCTGGGCACCTGTGAGCCACCCAGTTCCCGTGCAGCAATGGCTGCTGCATCGAC 1234
QY 249 AGTTTCCTGGAGTGTGACGACACCCCAAACTGCCCGCGCTCCGACGAGGCTGCCCTGT 308
Db 1235 AGTTTCCTGGAGTGTGACGACACCCCAAACTGCCCGCGCTCCGACGAGGCTGCCCTGT 1294
QY 309 GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGCAGCGACAAAGGG 368
Db 1295 GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGCAGCGACAAAGGG 1354
QY 369 CACTGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 428
Db 1355 CACTGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 1414
QY 429 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGTTGGTTGTTACGGCAACAAGAAC 488
Db 1415 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGTTGGTTGTTATGGCAACAAGAAC 1474
QY 489 AACTTTGAGGAAGAGCAGCGAGTGCCTCGAGTCTTGTGCGGCGCATCTCCAAAGAGGATGTG 548
Db 1475 AACTTTGAGGAAGAGCAGCGAGTGCCTCGAGTCTTGTGCGGCGCATCTCCAAAGAGGATGTG 1534
QY 549 TTTGGCCTGAGGCGGGAATCCCAATTCAGCAGCAGGCTCTGTGGAGATGGCTGTGCA 608
Db 1535 TTTGGCCTGAGGCGGGAATCCCAATTCAGCAGCAGGCTCTGTGGAGATGGCTGTGCA 1594
QY 609 GTGTTCTCTGTGTCATCTGCATTGTGGTGGTGTAGCCATCTTGGGTTTACTGCTTCTTCAAG 668
Db 1595 GTGTTCTCTGTGTCATCTGCATTGTGGTGGTGTAGCCATCTTGGGTTTACTGCTTCTTCAAG 1654
QY 669 AACCCAGAGAAAGGACTTCCACGGACACACACCCACCCACCCACCCACCCACCCCTGCCAGCTCC 728
Db 1655 AACCCAGAGAAAGGACTTCCACGGACACACACCCACCCACCCACCCACCCCTGCCAGCTCC 1714
QY 729 ACTGTCTCCACTACCGAGGACACGGAGGACCTGTCTATAACACACACCCGCGGCCCTC 788
Db 1715 ACTGTCTCCACTACCGAGGACACGGAGGACCTGTCTATAACACACACCCGCGGCCCTC 1774
QY 789 TGAGCCTGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTCTGCTTCCCAAGGCGAGGCC 848
Db 1775 TGAGCCTGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTCTGCTTCCCAAGGCGAGGCC 1834
QY 849 TGGGCTGGGAAAAACTTTGGAAACAGACTCTTGGCCCTGTTTCCAGGCGCCACTGTGCCTCA 908
Db 1835 TGGGCTGGGAAAAACTTTGGAAACAGACTCTTGGCCCTGTTTCCAGGCGCCACTGTGCCTCA 1894
QY 909 GAGACCAGGGCTCCAGCCCTCTTTGGAGAGTCTCAGCTAAGCTCAGTCTGAGAAAGC 968
Db 1895 GAGACCAGGGCTCCAGCCCTCTTTGGAGAGTCTCAGCTAAGCTCAGTCTGAGAAAGC 1954
QY 969 TCAAAGGTTTGGAGGAGCAGAAACCCCTTGGGCCAGAAAGTACCAGACTAGATGGACCTG 1028
Db 1955 TCAAAGGTTTGGAGGAGCAGAAACCCCTTGGGCCAGAAAGTACCAGACTAGATGGACCTG 2014
QY 1029 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTCTCTGTTCAAAGTGCCTGTCC 1088
Db 2015 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTCTCTGTTCAAAGTGCCTGTCC 2074
QY 1089 CTACCCCATGGTGTAGCAAGAGGAGTGGGGTGTGAGACCCCTGGAGGCCCAACCCCT 1148

DB	1955	TCAAAGGTTTGAAGGAGCAGAAAACCCCTTGGCCAGAACTACAGACTAGATGGACCTG	2014
QY	1029	CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTCTTCTCTGTTCAAAGCTGCCTGTCC	1088
DB	2015	CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTCTTCTCTGTTCAAAGCTGCCTGTCC	2074
QY	1089	CTACCCCATGGTGCTAGGAAGAGGAGTGGGGTGGTGTCTAGACCCCTGGAGGCCCCCAACCCCT	1148
DB	2075	CTACCCCATGGTGCTAGGAAGAGGAGTGGGGTGGTGTCTAGACCCCTGGAGGCCCCCAACCCCT	2134
QY	1149	GTCTCTCCGAGCTCTCTTCCATGCTGTGCGGCCAGGGCTGGGAGGAAGGACTTCCCTGT	1208
DB	2135	GTCTCTCCGAGCTCTCTTCCATGCTGTGCGGCCAGGGCTGGGAGGAAGGACTTCCCTGT	2194
QY	1209	GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTGTTATTTAATGCTGTGGCATGGTGAAGAG	1268
DB	2195	GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTGTTATTTAATGCTGTGGCATGGTGAAGAG	2254
QY	1269	GAGGGGAAGAGGCTGTTTGGCCTCTCTATCCTCTCTTCTCTTCTTCCCCCAAGATTGAGCT	1328
DB	2255	GAGGGGAAGAGGCTGTTTGGCCTCTCTGTCTCTCTCTTCTTCTTCCCCCAAGATTGAGCT	2314
QY	1329	CTCTGCCCTTGATCAGCCCCACCCCTGGCCTAGACCAGCAGACAGAGCCAGGAGAAGCTCA	1388
DB	2315	CTCTGCCCTTGATCAGCCCCACCCCTGGCCTAGACCAGCAGACAGAGCCAGGAGAAGCTCA	2374
QY	1389	GCTGCATTCCGACGCCCCCACCCCAAGGTTCTCCAAACATCACAGCCCCAGCCGCCCCACT	1448
DB	2375	GCTGCATTCCGACGCCCCCACCCCAAGGTTCTCCAAACATCACAGCCCCAGCCGCCCCACT	2434
QY	1449	GGGTAATAAAGTGGTTGTGGAAAAAATAAAAAAATAAAAAA	1492
DB	2435	GGGTAATAAAGTGGTTGTGGAAAAAATAAAAAAATAAAAAA	2478

RESULT 5

US-10-245-859-9
Sequence 9, Application US/10245859
Publication No. US20030064474A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C78
CURRENT APPLICATION NUMBER: US/10/245,859
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801

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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-859-9

Query Match      97.5%; Score 1468; DB 13; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 9 CACGAGCAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAAAC 68
Db 995 CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAAAC 1054

QY 69 TACCTTCGGGAAGAAGAGTGCATTTCTAGCCTGTTCGGGCTGTCAAGGTGGGCTTTTGAGA 128
Db 1055 TACCTTCGGGAAGAAGAGTGCATTTCTAGCCTGTTCGGGCTGTCAAGGTGGGCTTTTGAGA 1114

QY 129 GGCAGCTCTGGGGCTCAGGCGACTTCCCCAGGGCCCTCCATGGAAGGCCCATCCA 188
Db 1115 GGCAGCTCTGGGGCTCAGGCGACTTCCCCAGGGCCCTCCATGGAAGGCCCATCCA 1174

QY 189 GTGTGCTCTGGCACCTGTTCAGGCCACCCAGTTCGCGTGCAGCAATGGCTGTGCATCGAC 248
Db 1175 GTGTGCTCTGGCACCTGTTCAGGCCACCCAGTTCGCGTGCAGCAATGGCTGTGCATCGAC 1234

QY 249 AGTTTCTCTGGAGTGTGACGACACCCCAACTGCCCGACGCCTCCAGCAGGCTGCCTGT 308
Db 1235 AGTTTCTCTGGAGTGTGACGACACCCCAACTGCCCGACGCCTCCAGCAGGCTGCCTGT 1294

QY 309 GAAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCGACAAGGG 368
Db 1295 GAAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCGACAAGGG 1354

QY 369 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 428
Db 1355 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 1414

QY 429 AACCCCTTCAGCGAACAACCTGCGCCCGCTTTACCTATGGTGGTTGTTTACGGCAACAAGAAC 488
Db 1415 AACCCCTTCAGCGAACAACCTGCGCCCGCTTTACCTATGGTGGTTGTTTATGCGCAACAAGAAC 1474

QY 489 AACTTTGAGGAAGAGCAGAGTGCCTCGAGTCTTGTTCGGGCATCTCCAGAGAGGATGTG 548
Db 1475 AACTTTGAGGAAGAGCAGAGTGCCTCGAGTCTTGTTCGGGCATCTCCAGAGAGGATGTG 1534

QY 549 TTTTGGCTGAGGCGGGAATCCCATTTCCAGCACAGGCTCTGTGGAGATGGCTGTGCGCA 608
Db 1535 TTTTGGCTGAGGCGGGAATCCCATTTCCAGCACAGGCTCTGTGGAGATGGCTGTGCGCA 1594

QY 609 GTGTTCTCTGGTCACTCTGCATTTGGTGGTGGTAGCCATCTTTGGGTTACTGCTTCTTCAAG 668
Db 1595 GTGTTCTCTGGTCACTCTGCATTTGGTGGTGGTAGCCATCTTTGGGTTACTGCTTCTTCAAG 1654

QY 669 AACGAGAGAAAGGACTTCCAGGACACCAACCCACCCACCCACCCCTGCCAGCTCC 728
Db 1655 AACGAGAGAAAGGACTTCCAGGACACCAACCCACCCACCCACCCCTGCCAGCTCC 1714

QY 729 ACTGTCTCCACTACCGAGGACACGGAGCACTTGTGTTCTATACCACACCGCGGCCCTC 788
Db 1715 ACTGTCTCCACTACCGAGGACACGGAGCACTTGTGTTCTATACCACACCGCGGCCCTC 1774

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Db 1775 TGAGCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTGCTTCCCAAGGCAGAGGCC 1834

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QY	729	ACTGTCTCCA	CTACCGAGGACACGGAGCACCTGGTCTATAAACCAACACACCGGCGCCCTC	788
Db	1715	ACTGTCTCCA	CTACCGAGGACACGGAGCACCTGGTCTATAAACCAACACACCGGCGCCCTC	1774
QY	789	TGAGCCTGGG	CTCACCGGCTCTCACCTGGCCCTGCTTCTGTCTGCCAAGGCAGAGGCC	848
Db	1775	TGAGCCTGGG	CTCACCGGCTCTCACCTGGCCCTGCTTCTGTCTGCCAAGGCAGAGGCC	1834
QY	849	TGGGCTGGG	AAAACTTTGGAAACAGACTCTTGCCCTGTGTTCCAGGCCCACTGTGCCTCA	908
Db	1835	TGGGCTGGG	AAAACTTTGGAAACAGACTCTTGCCCTGTGTTCCAGGCCCACTGTGCCTCA	1894
QY	909	GAGACCA	GGGCTCCAGGCCCTCTTGGAGAACTCTCAGCTAAGCTCACGTCCTGAGAAAAGC	968
Db	1895	GAGACCA	GGGCTCCAGGCCCTCTTGGAGAACTCTCAGCTAAGCTCACGTCCTGAGAAAAGC	1954
QY	969	TCAAAGG	TTTGGAAAGCAGAAAAACCTTTGGGCCAGAAAGTACAGACTAGATGGACCTG	1028
Db	1955	TCAAAGG	TTTGGAAAGCAGAAAAACCTTTGGGCCAGAAAGTACAGACTAGATGGACCTG	2014
QY	1029	CCTGCAT	AGGAGTTTGGAGGAAGTTGGAGTTTGTGTTTCTCTGTTTCAAAGCTGCCTGTCC	1089
Db	2015	CCTGCAT	AGGAGTTTGGAGGAAGTTGGAGTTTGTGTTTCTCTGTTTCAAAGCTGCCTGTCC	2074
QY	1089	CTACCCCA	TGCTAGGAAGAGGTGGGTGGTGTCTAGACCCCTGGAGGCCCAACCCCT	1148
Db	2075	CTACCCCA	TGCTAGGAAGAGGTGGGTGGTGTCTAGACCCCTGGAGGCCCAACCCCT	2134
QY	1149	GTCCTCC	CGAGCTCCTCTTCCATGCTGTGCGCCCAAGGCTGGGAGGAAGACTTCCCTGT	1208
Db	2135	GTCCTCC	CGAGCTCCTCTTCCATGCTGTGCGCCCAAGGCTGGGAGGAAGACTTCCCTGT	2194
QY	1209	GTAGTTTG	TGCTGTAAAGAGTTGCTTTTGTGTTTATTTAATGCTGTGGCATGGGTGAAGAG	1268
Db	2195	GTAGTTTG	TGCTGTAAAGAGTTGCTTTTGTGTTTATTTAATGCTGTGGCATGGGTGAAGAG	2254
QY	1269	GAGGGA	AGAGGCCCTGTTTGGCCCTCTCTATCTCTCTTCTTCTTCCCCAAGATTGAGCT	1328
Db	2255	GAGGGA	AGAGGCCCTGTTTGGCCCTCTCTATCTCTCTTCTTCTTCCCCAAGATTGAGCT	2314
QY	1329	CTCTG	CCCTTGATCAGCCCCACCCCTGGCCTAGACCAGCAGACAGGCCAGGAGGCTCA	1388
Db	2315	CTCTG	CCCTTGATCAGCCCCACCCCTGGCCTAGACCAGCAGACAGGCCAGGAGGCTCA	2374
QY	1389	GCTGCAT	TCCGAGCCCCCAACCCCAAGTTTCTCCAACATCACAGCCAGCCCGCCCACT	1448
Db	2375	GCTGCAT	TCCGAGCCCCCAACCCCAAGTTTCTCCAACATCACAGCCAGCCCGCCCACT	2434
QY	1449	GGGTAA	TAAAAGTGGTTGTGGAAAAAAGAAAAAAGAAAAA	1492
Db	2435	GGGTAA	TAAAAGTGGTTGTGGAAAAAAGAAAAAAGAAAAA	2478

RESULT 7

US-10-305-654-41
; Sequence 41, Application US/10305654
; Publication No. US20030224984A1

; GENERAL INFORMATION:

APPLICANT:	Baker, Kevin P.
APPLICANT:	Ferrara, Napoleone
APPLICANT:	Gerber, Hans-Peter
APPLICANT:	Gerritsen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Gurney, Austin L.
APPLICANT:	Hillan, Kenneth J.
APPLICANT:	Marsters, Scot A.
APPLICANT:	Pan, J.
APPLICANT:	Paoni, N. F.
APPLICANT:	Stephan, J-P F.
APPLICANT:	Watanabe, C.K.
APPLICANT:	Wood, W.I.

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; APPLICANT: Williams, P.M.
; APPLICANT: Ye. Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235R1C1
; CURRENT APPLICATION NUMBER: US/10/305,654
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 41
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homosapiens
US-10-305-654-41

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Query Match	97.5%;	Score 1468;	DB 13;	Length 2482;	
Best Local Similarity	99.3%;	Pred. No. 0;			
Matches 1474;	Conservative	0;	Mismatches 10;	Indels 0;	Gaps 0;
Qy	9	CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGAGGCTGCTTGGGCAACAAGAACAAAC	68		
Db	995	CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGAGGCTGCTTGGGCAACAAGAACAAAC	1054		
Qy	69	TACCTTCGGGAAGAGAGTGCAATCTAGCCTGTTCGGGGTGTGCAAGGTGGGCTTTTGAGA	128		
Db	1055	TACCTTCGGGAAGAGAGTGCAATCTAGCCTGTTCGGGGTGTGCAAGGTGGGCTTTTGAGA	1114		
Qy	129	GGCAGCTCTGGGGCTCAGGCGACTTTCCTCCAGGGGCCCTCCATGAAAGGCGCCATCCA	188		
Db	1115	GGCAGCTCTGGGGCTCAGGCGACTTTCCTCCAGGGGCCCTCCATGAAAGGCGCCATCCA	1174		
Qy	189	GTGTGCTCTGGCACCTGTGAGCCACCCAGTTCGCTCGAGCAATGGCTGTGCATCGAC	248		
Db	1175	GTGTGCTCTGGCACCTGTGAGCCACCCAGTTCGCTCGAGCAATGGCTGTGCATCGAC	1234		
Qy	249	AGTTTCCTGGAGGTGACGACACCCCACTGCCCCGACGCCCTCCGACGAGGCTGCCTGT	308		
Db	1235	AGTTTCCTGGAGGTGACGACACCCCACTGCCCCGACGCCCTCCGACGAGGCTGCCTGT	1294		
Qy	309	GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCGACAAAGGG	368		
Db	1295	GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGTGACAAAGGG	1354		
Qy	369	CACCTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC	428		
Db	1355	CACCTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC	1414		
Qy	429	AACCCCTTCAGCGAACACTGCGCCCCGCTTACCTATGGTGGTTGTTACGGCAACAAGAAC	488		
Db	1415	AACCCCTTCAGCGAACACTGCGCCCCGCTTACCTATGGTGGTTGTTATGGCAACAAGAAC	1474		
Qy	489	AACCTTTGAGGAAGACAGCAGTGCCTCGAGTCTTGTTCGGGCATCTCCAGAAGGATGTG	548		
Db	1475	AACCTTTGAGGAAGACAGCAGTGCCTCGAGTCTTGTTCGGGCATCTCCAGAAGGATGTG	1534		
Qy	549	TTTGGCCTGAGCGGGAAATCCCCATTCCAGCACAGGCTCTGTGGAGATGGCTGTGCA	608		
Db	1535	TTTGGCCTGAGCGGGAAATCCCCATTCCAGCACAGGCTCTGTGGAGATGGCTGTGCA	1594		
Qy	609	GTGTTCTTGTCATCTGCATTGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG	668		
Db	1595	GTGTTCTTGTCATCTGCATTGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG	1654		
Qy	669	AACCAGAGAAAGGACTTCCACGGACACCAACACACCCACCAACCCCTGCCAGCTCC	728		
Db	1655	AACCAGAGAAAGGACTTCCACGGACACCAACACACCCACCAACCCCTGCCAGCTCC	1714		
Qy	729	ACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCAACCAACCGCGGCCCTC	788		
Db	1715	ACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCAACCAACCGCGGCCCTC	1774		
Qy	789	TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTCTGCTTGCACAGGACGGCC	848		
Db	1775	TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTCTGCTTGCACAGGACGGCC	1834		

QY 849 TGGGCTGGGAAAAAATTTGGAAACAGACTCTTGGCCTGTTTCCAGGCGCCACTGTGCCTCA 908
DB 1835 TGGGCTGGGAAAAAATTTGGAAACAGACTCTTGGCCTGTTTCCAGGCGCCACTGTGCCTCA 1894
QY 909 GAGACAGGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGCTCCTCTGAGAAAGC 968
DB 1895 GAGACAGGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGCTCCTCTGAGAAAGC 1954
QY 969 TCAAGGTTTGGAGAGCAGAAACCCCTTGGCCAGAGTACAGACTAGATGAGACCTG 1028
DB 1955 TCAAGGTTTGGAGAGCAGAAACCCCTTGGCCAGAGTACAGACTAGATGAGACCTG 2014
QY 1029 CCTGCATAGAGTTGGAGAGTGGAGTTTGGAGTTTCTCTCTGTTCAAGCTGCCTGTCC 1088
DB 2015 CCTGCATAGAGTTGGAGAGTGGAGTTTGGAGTTTCTCTCTGTTCAAGCTGCCTGTCC 2074
QY 1089 CTACCCCATGGTGTAGGAAGAGAGTGGGGTGTGAGACCCCTGGAGGCCCCCAACCT 1148
DB 2075 CTACCCCATGGTGTAGGAAGAGAGTGGGGTGTGAGACCCCTGGAGGCCCCCAACCT 2134
QY 1149 GTCTCTCCGAGCTCCTCTTCCATGCTGTGCGCCAGGGCTGGAGGAGGAGTCCCTGT 1208
DB 2135 GTCTCTCCGAGCTCCTCTTCCATGCTGTGCGCCAGGGCTGGAGGAGGAGTCCCTGT 2194
QY 1209 GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTGTTTAAATGCTGTGGCATGGGTGAAGAG 1268
DB 2195 GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTGTTTAAATGCTGTGGCATGGGTGAAGAG 2254
QY 1269 GAGGGGAAGAGGCGCTTGTGGCCTCTCTAFCCTCTCTTCTCTTCCCCAAGATTGAGCT 1328
DB 2255 GAGGGGAAGAGGCGCTTGTGGCCTCTCTGFCCTCTCTTCTCTTCCCCAAGATTGAGCT 2314
QY 1329 CTCTGCCCTTGATCAGCCCCACCTGGCCTTAGCCAGCAGACAGAGCCAGGAGAGCTCA 1388
DB 2315 CTCTGCCCTTGATCAGCCCCACCTGGCCTTAGCCAGCAGACAGAGCCAGGAGAGCTCA 2374
QY 1389 GCTGCATTCCGAGCGCCCGCCACCCCAAGGTTCTCCAAATCATCAGCCCGGCCCACT 1448
DB 2375 GCTGCATTCCGAGCGCCCGCCACCCCAAGGTTCTCCAAATCATCAGCCCGGCCCACT 2434
QY 1449 GGGTAATAAAGTGGTTTGTGGAAAAAATAAATAAATAAATAA 1492
DB 2435 GGGTAATAAAGTGGTTTGTGGAAAAAATAAATAAATAAATAA 2478

RESULT 8
US-10-245-103-9
; Sequence 9, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C112
; CURRENT APPLICATION NUMBER: US/10/245,103
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046

; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-245-103-9

Query Match 97.5%; Score 1468; DB 15; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAAC 68
DB 995 CCCACGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAAC 1054
QY 69 TACCTTCGGGAAGAAGAGTGCATTTCTAGCCTGTGCGGGTGTGCAAGTGGGCTTTGAGA 128
DB 1055 TACCTTCGGGAAGAAGAGTGCATTTCTAGCCTGTGCGGGTGTGCAAGTGGGCTTTGAGA 1114
QY 129 GGCAGCTCTGGGGCTCAGGCGACTTTCCCTCCAGGCGCCCTCCATGGAAGGCGCCATCCA 188
DB 1115 GGCAGCTCTGGGGCTCAGGCGACTTTCCCTCCAGGCGCCCTCCATGGAAGGCGCCATCCA 1174
QY 189 GTGTGCTCTGGCACCTGTGTCAGCCCAAGCTTCCGCTGTCAGCAATGGCTGCTGCATGAC 248
DB 1175 GTGTGCTCTGGCACCTGTGTCAGCCCAAGCTTCCGCTGTCAGCAATGGCTGCTGCATGAC 1234
QY 249 AGTTTCCTGAGTGTGACGACACCCCAAGCTTCCGCTGTCAGCAATGGCTGCTGCATGAC 308
DB 1235 AGTTTCCTGAGTGTGACGACACCCCAAGCTTCCGCTGTCAGCAATGGCTGCTGCATGAC 1294
QY 309 GAAAAATACAGAGTGGCTTTGACGAGTCCAGCGCATCCATTTCCCGAGCGCAAGAGG 368
DB 1295 GAAAAATACAGAGTGGCTTTGACGAGTCCAGCGCATCCATTTCCCGAGCGCAAGAGG 1354
QY 369 CACTGCTGACCTGTCAGACACAGAGTCTGCAAGGAGAGCATCCCGCTGCTGTACTAC 428
DB 1355 CACTGCTGACCTGTCAGACACAGAGTCTGCAAGGAGAGCATCCCGCTGCTGTACTAC 1414
QY 429 AACCCCTTCAGCGAACACTGCGCCGCTTTTACCTATGTTGTTGTAGCGCAACAAGAAC 488
DB 1415 AACCCCTTCAGCGAACACTGCGCCGCTTTTACCTATGTTGTTGTATGGCAACAAGAAC 1474
QY 489 AACTTTGAGGAAGAGCAGTGCCTCGAGTCTTGTGCGGCACTCTCCAAAGAGGATGTG 548
DB 1475 AACTTTGAGGAAGAGCAGTGCCTCGAGTCTTGTGCGGCACTCTCCAAAGAGGATGTG 1534
QY 549 TTTGGCCTGAGCGGGAATCCCAATTCAGCAGCAGGCTCTGTGGAGATGCTGTGCA 608
DB 1535 TTTGGCCTGAGCGGGAATCCCAATTCAGCAGCAGGCTCTGTGGAGATGCTGTGCA 1594
QY 609 GTGTTCTCTGCTCATCTGCTATTGTGGTGGTGTAGCCATCTTGGTGTACTGCTTCTCAAG 668
DB 1595 GTGTTCTCTGCTCATCTGCTATTGTGGTGGTGTAGCCATCTTGGTGTACTGCTTCTCAAG 1654
QY 669 AACGAGAGAAAGACTTCCAGGACACCAACCAACCAACCAACCAACCAACCAACCAAC 728

DB	1535	TTTGGCCTGAGGGGGGAAATCCCCATTCCACGACACAGGCTCTGTGGAGATGGCTGTCA	1594
QY	609	GTGTTCCCTGGTCACTGTCATTTGTGATGTTGGTAGCCATCTTTGGGTACTGCTTCTTCAAG	668
DB	1595	GTGTTCCCTGGTCACTGTCATTTGTGATGTTGGTAGCCATCTTTGGGTACTGCTTCTTCAAG	1654
QY	669	AACCAGAGAAAGGACTTCCACGGACACCAACCACCCACCCACCCACCCCTGCCAGTCC	728
DB	1655	AACCAGAGAAAGGACTTCCACGGACACCAACCACCCACCCACCCACCCCTGCCAGTCC	1714
QY	729	ACTGCTCCACTACCGAGGACACGGAGCACCTGGTCTATTAACCAACCAACCGCGGCCCTC	788
DB	1715	ACTGCTCCACTACCGAGGACACGGAGCACCTGGTCTATTAACCAACCAACCGCGGCCCTC	1774
QY	789	TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCCTGCTTGCCTTGCCTTGCAGAGGCC	848
DB	1775	TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCCTGCTTGCCTTGCCTTGCAGAGGCC	1834
QY	849	TGGGCTGGGAAAAACTTTGGNACCAGACTCTTGCCCTGTTTTCCAGGCCCACTGTGCTCA	908
DB	1835	TGGGCTGGGAAAAACTTTGGNACCAGACTCTTGCCCTGTTTTCCAGGCCCACTGTGCTCA	1894
QY	909	GAGACCAAGGCTCCAGCCCTCTTTGGAGAACTCTCAGCTAAGCTCAGTCTCTGAGAAAGC	968
DB	1895	GAGACCAAGGCTCCAGCCCTCTTTGGAGAACTCTCAGCTAAGCTCAGTCTCTGAGAAAGC	1954
QY	969	TCAAAGGTTTGGAGGACAGAAAAACCTTTGGGCCCAGAAGTACCAGACTAGATGGACCTG	1028
DB	1955	TCAAAGGTTTGGAGGACAGAAAAACCTTTGGGCCCAGAAGTACCAGACTAGATGGACCTG	2014
QY	1029	CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTCTCTCTGTTCAAAGCTGCTGTGCC	1088
DB	2015	CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTCTCTCTGTTCAAAGCTGCTGTGCC	2074
QY	1089	CTACCCCATGGTCTAGGAAGAGGAGTGGGGTGGTGTCTAGACCCCTGGAGGCCCAACCTT	1148
DB	2075	CTACCCCATGGTCTAGGAAGAGGAGTGGGGTGGTGTCTAGACCCCTGGAGGCCCAACCTT	2134
QY	1149	GTCCTCCCGAGCTCCTCTTCCATGCTGTGGCCCAAGGCTGGGAGGGAAGCACTTCCCTGT	1208
DB	2135	GTCCTCCCGAGCTCCTCTTCCATGCTGTGGCCCAAGGCTGGGAGGGAAGCACTTCCCTGT	2194
QY	1209	GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTGTTTATTAATGCTGTGGCATGGGTGAAGAG	1268
DB	2195	GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTGTTTATTAATGCTGTGGCATGGGTGAAGAG	2254
QY	1269	GAGGGGAAGAGGCTGTTTGGCCTCTCTATCTCTCTTCTCTTCCCCCAAGATTGAGCT	1328
DB	2255	GAGGGGAAGAGGCTGTTTGGCCTCTCTATCTCTCTTCTCTTCCCCCAAGATTGAGCT	2314
QY	1329	CTCTGCCCTTGATCAGCCCCCAACCTTGGCCTAGACAGAGCAGACAGAGCCAGGAGAAGCTCA	1388
DB	2315	CTCTGCCCTTGATCAGCCCCCAACCTTGGCCTAGACAGAGCAGACAGAGCCAGGAGAAGCTCA	2374
QY	1389	GCTGCATTCCGAGCCCCCAACCTTGGAGGTTCTCAACATCACAGCCCCAGCCCCCACT	1448
DB	2375	GCTGCATTCCGAGCCCCCAACCTTGGAGGTTCTCAACATCACAGCCCCAGCCCCCACT	2434
QY	1449	GGGTAATAAAGTGGTTGTGGAAAAAATAAAAAAAAAAAAAAAAAAAAAA	1492
DB	2435	GGGTAATAAAGTGGTTGTGGAAAAAATAAAAAAAAAAAAAAAAAAAAAA	2478

309	GA	AAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCGACAAAGGG	368
	QY		
1295	GA	AAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGTGACAAAGGG	1354
	Db		
369	CA	CTGCGTGGACCTGCCAGACACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC	428
	QY		
1355	CA	CTGCGTGGACCTGCCAGACACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC	1414
	Db		

; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Phillippe
 ; APPLICANT: Watanabe, Colin
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; APPLICANT: Fong, Sherman
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3630R1C90
 ; CURRENT APPLICATION NUMBER: US/10/245,143
 ; PRIOR FILING DATE: 2002-09-16
 ; PRIOR FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/059114
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/063046
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/065027
 ; PRIOR FILING DATE: 1997-11-10
 ; PRIOR APPLICATION NUMBER: 60/079689
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/086478
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087607
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/089801
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/090557
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090689
 ; PRIOR FILING DATE: 1998-06-25
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 116

Query Match 97.5%; Score 1468; DB 15; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474: Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	9	CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGAGAGCGTCTGTTGGGCAACAAGAACAAAC	68
Db	995	CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGAGAGCGTCTGTTGGGCAACAAGAACAAAC	1054
QY	69	TACCTTCGGGAAGAAGATGCATTCTAGCCCTGTCGGGGTGTGCAAGGTGGGCCCTTTTGAGA	128
Db	1055	TACCTTCGGGAAGAAGATGCATTCTAGCCCTGTCGGGGTGTGCAAGGTGGGCCCTTTTGAGA	1114
QY	129	GGCAGCTCTGGGGCTCAGGCGGACTTTCCCCCAGGGCCCCCTCCATGGAAAGGCGCCATCCA	188
Db	1115	GGCAGCTCTGGGGCTCAGGCGGACTTTCCCCCAGGGCCCCCTCCATGGAAAGGCGCCATCCA	1174
QY	189	GTGTGCTCTGGCACTGTGAGCCCAACCCAGTTCCGCTGCAGCAATGGCTGCTGCATCGAC	248
Db	1175	GTGTGCTCTGGCACTGTGAGCCCAACCCAGTTCCGCTGCAGCAATGGCTGCTGCATCGAC	1234
QY	249	AGTTTCTTGAGTGTGACGACACCCCCCAACTGCCCCGACGCCCTCCGACGAGGGTGCCTGT	308
Db	1235	AGTTTCTTGAGTGTGACGACACCCCCCAACTGCCCCGACGCCCTCCGACGAGGGTGCCTGT	1294
QY	309	GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTCCCCAGCGACAAAGGG	368
Db	1295	GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTCCCCAGCGACAAAGGG	1354
QY	369	CAC TCGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC	428
Db	1355	CAC TCGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC	1414

QY 429 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGTTGGTTGTTTACGGCAACAAGAAC 488
Db 1415 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGTTGGTTGTTTATGGCAACAAGAAC 1474
QY 489 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGGCATCTCCAAGAAGGATGTG 548
Db 1475 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGGCATCTCCAAGAAGGATGTG 1534
QY 549 TTGGCCCTGAGCGCGGAAATCCCATTTCCAGCACAGGCTCTGTGGAGATGGCTGTGCGCA 608
Db 1535 TTGGCCCTGAGCGCGGAAATCCCATTTCCAGCACAGGCTCTGTGGAGATGGCTGTGCGCA 1594
QY 609 GTGTTCCCTGGTCACTGTGATTGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 668
Db 1595 GTGTTCCCTGGTCACTGTGATTGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 1654
QY 669 AACAGAGAAAGGACTTCCACGGACACCGGACACCCACCCACCCACCCACCCCTGCCAGCTCC 728
Db 1655 AACAGAGAAAGGACTTCCACGGACACCGGACACCCACCCACCCACCCACCCCTGCCAGCTCC 1714
QY 729 ACTGTCTCACTACCGAGGACACCGGACACCTGGTCTATATAACACACACCGCGGCCCTTC 788
Db 1715 ACTGTCTCACTACCGAGGACACCGGACACCTGGTCTATATAACACACACCGCGGCCCTTC 1774
QY 789 TGAGCCTGGTCTCAACCGCTCTCACTGGCCCTGCTTCTGCTTCCAGGCCCCACTGTGCTCA 848
Db 1775 TGAGCCTGGTCTCAACCGCTCTCACTGGCCCTGCTTCTGCTTCCAGGCCCCACTGTGCTCA 1834
QY 849 TGGGCTGGGAAAAAATTGGAACACAGACTTTGCCCTGTTTCCAGGCCCCACTGTGCTCA 908
Db 1835 TGGGCTGGGAAAAAATTGGAACACAGACTTTGCCCTGTTTCCAGGCCCCACTGTGCTCA 1894
QY 909 GAGACAGGGCTCCAGCCCTCTTGGAGAACTCTCAGCTAAGCTCACGTCTCTGAGAAAGC 968
Db 1895 GAGACAGGGCTCCAGCCCTCTTGGAGAACTCTCAGCTAAGCTCACGTCTCTGAGAAAGC 1954
QY 969 TCAAAGTTTGGAGGAGCAGAAACCTTGGGCCAGAGTACAGACTAGATGGACCTG 1028
Db 1955 TCAAAGTTTGGAGGAGCAGAAACCTTGGGCCAGAGTACAGACTAGATGGACCTG 2014
QY 1029 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTTCAAAGTGCCTGTCC 1088
Db 2015 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTTCAAAGTGCCTGTCC 2074
QY 1089 CTACCCCATGCTGTAGGAAGAGGAGTGGGGTGGTGTGTCAGACCCCTGGAGGCCCAACCCCT 1148
Db 2075 CTACCCCATGCTGTAGGAAGAGGAGTGGGGTGGTGTGTCAGACCCCTGGAGGCCCAACCCCT 2134
QY 1149 GTCCTCCCGAGCTCCTCTTCCATGCTGTGCGCCCGAGGGCTGGGAGGAAGGACTTCCCTGT 1208
Db 2135 GTCCTCCCGAGCTCCTCTTCCATGCTGTGCGCCCGAGGGCTGGGAGGAAGGACTTCCCTGT 2194
QY 1209 GTAGTTTGTGCTGTAAGAGATTGCTTTTGTATTTAATGCTGTGGCATGGGTGAAGAG 1268
Db 2195 GTAGTTTGTGCTGTAAGAGATTGCTTTTGTATTTAATGCTGTGGCATGGGTGAAGAG 2254
QY 1269 GAGGGGAAGAGGCTGTTTGGCCCTCTCTATCCTCTCTTCCCTTCCCTTCCCTTCCCTTCCCT 1328
Db 2255 GAGGGGAAGAGGCTGTTTGGCCCTCTCTATCCTCTCTTCCCTTCCCTTCCCTTCCCTTCCCT 2314
QY 1329 CTCTGCCCTTGTATCAGCCCCACCTGGCCTAGACCCAGCAGACAGAGCCAGGAGAGCTCA 1388
Db 2315 CTCTGCCCTTGTATCAGCCCCACCTGGCCTAGACCCAGCAGACAGAGCCAGGAGAGCTCA 2374
QY 1389 GCTGCAATCCGAGCCCCACCCCCCAAGTTCTCCAACATCAACAGCCAGCCCGCCCACT 1448
Db 2375 GCTGCAATCCGAGCCCCACCCCCCAAGTTCTCCAACATCAACAGCCAGCCCGCCCACT 2434
QY 1449 GGGTAATAAAGTGGTTTGTGGAATAAATAAATAAATAAATAA 1492
Db 2435 GGGTAATAAAGTGGTTTGTGGAATAAATAAATAAATAAATAA 2478

RESULT 11
US-10-245-771-9
; Sequence 9, Application US/10245771
; Publication No. US20030068781A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C98
; CURRENT APPLICATION NUMBER: US/10/245,771
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-771-9

Query Match 97.5%; Score 1468; DB 15; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAC 68
Db 995 CCCACGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAC 1054
QY 69 TACCTTCGGGAAGAGAGTGCATTCTAGCCTGTGCGGGGTGTGCAAGGTGGGCTTTGAGA 128
Db 1055 TACCTTCGGGAAGAGAGTGCATTCTAGCCTGTGCGGGGTGTGCAAGGTGGGCTTTGAGA 1114
QY 129 GGCAGCTCTGGGGCTCAGGCGCACTTCCCGGAGGCTTCCATGGAAGGCGCCATCCA 188
Db 1115 GGCAGCTCTGGGGCTCAGGCGCACTTCCCGGAGGCTTCCATGGAAGGCGCCATCCA 1174
QY 189 GTGTGCTCTGGCACCTGTGAGCCCAACCCAGTTCCGCTGAGCAATGGCTGTGATCGAC 248
Db 1175 GTGTGCTCTGGCACCTGTGAGCCCAACCCAGTTCCGCTGAGCAATGGCTGTGATCGAC 1234
QY 249 AGTTTCTGGAGTGTGAGACACCCCACTGCCCGAGGCTCCGACGAGGCTGCTGT 308
Db 1235 AGTTTCTGGAGTGTGAGACACCCCACTGCCCGAGGCTCCGACGAGGCTGCTGT 1294

QY	309	GAAAAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCGCCAGCACAAAGGG	368
DB	1295	GAATAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCGCCAGCACAAAGGG	1354
QY	369	CACGCGTGGAACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCGCGCTGGTACTAC	428
DB	1355	CACGCGTGGAACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCGCGCTGGTACTAC	1414
QY	429	AACCCCTTCAGCGAACAACCTGCGCCCGCTTTACTATATGGTGTGTTACGCAACAAGAAC	488
DB	1415	AACCCCTTCAGCGAACAACCTGCGCCCGCTTTACTATATGGTGTGTTATGCAACAAGAAC	1474
QY	489	AACCTTTGAGGAACAGCAGAGTGCCTCGAGTCTTGTGCGGCACTCTCCAAGAAGGATGTG	548
DB	1475	AACCTTTGAGGAACAGCAGAGTGCCTCGAGTCTTGTGCGGCACTCTCCAAGAAGGATGTG	1534
QY	549	TTTGGCCTGAGCGGGAATCCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTGCA	608
DB	1535	TTTGGCCTGAGCGGGAATCCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTGCA	1594
QY	609	GTGTTCCCTGGTCACTCTGCATTGTGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTAAG	668
DB	1595	GTGTTCCCTGGTCACTCTGCATTGTGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTAAG	1654
QY	669	AACCAGAGAAAGACTTCCACGGACACCAACCAACCCACCCCTGCGAGCTCC	728
DB	1655	AACCAGAGAAAGACTTCCACGGACACCAACCAACCCACCCCTGCGAGCTCC	1714
QY	729	ACTGTCTCCACTAACCGAGGACACGGAGCACCTGGTCTATAACCAACCAACCGGCCCCCTC	788
DB	1715	ACTGTCTCCACTAACCGAGGACACGGAGCACCTGGTCTATAACCAACCAACCGGCCCCCTC	1774
QY	789	TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTGTCTTGCCTGCTGCTGCTCA	848
DB	1775	TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTGTCTTGCCTGCTGCTGCTCA	1834
QY	849	TGGGCTGGGAAAACCTTTGGAACCAAGACTCTTGGCTGTTTTCCAGGCCCACTGTGCTCA	908
DB	1835	TGGGCTGGGAAAACCTTTGGAACCAAGACTCTTGGCTGTTTTCCAGGCCCACTGTGCTCA	1894
QY	909	GAGACCAGGGCTCCAGCCCCCTCTTGGAGAACTCTCAGCTAAGCTCACTGCTGAGAAAGC	968
DB	1895	GAGACCAGGGCTCCAGCCCCCTCTTGGAGAACTCTCAGCTAAGCTCACTGCTGAGAAAGC	1954
QY	969	TCAAAGGTTTGGAGGAGCAGAAAACCTTGGGCCAGAAAGTACCAGACTAGATGGACCTG	1028
DB	1955	TCAAAGGTTTGGAGGAGCAGAAAACCTTGGGCCAGAAAGTACCAGACTAGATGGACCTG	2014
QY	1029	CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTTGTTTCTCTGTTTCAAAGCTGCTGTCC	1088
DB	2015	CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTTGTTTCTCTGTTTCAAAGCTGCTGTCC	2074
QY	1089	CTACCCCATGGTCTAGGAAGAGGAGTGGGTGGTGTCCAGACCTGGAGGCCCAACCTT	1148
DB	2075	CTACCCCATGGTCTAGGAAGAGGAGTGGGTGGTGTCCAGACCTGGAGGCCCAACCTT	2134
QY	1149	GTCCTCCOGAGCTCCTCTTCCATGCTGTGCGCCCAAGSCTGGGAGGAAGGACTTCCCTGT	1208
DB	2135	GTCCTCCOGAGCTCCTCTTCCATGCTGTGCGCCCAAGSCTGGGAGGAAGGACTTCCCTGT	2194
QY	1209	GTAGTTTGTGCTGTAACAGTTGCTTTTTTGTATTAATGCTGTGGCATGGGTGAAGAG	1268
DB	2195	GTAGTTTGTGCTGTAACAGTTGCTTTTTTGTATTAATGCTGTGGCATGGGTGAAGAG	2254
QY	1269	GAGGGGAAGAGGCTGTTTGGCCTCTCTATCCTCTTCTCTTCCCCCAAGATTGAGCT	1328
DB	2255	GAGGGGAAGAGGCTGTTTGGCCTCTCTATCCTCTTCTCTTCCCCCAAGATTGAGCT	2314
QY	1329	CTCTGCCCTTGATCAGCCCCCACTGGCCTAGACCCAGCAGACAGAGCAGGAGAGCTCA	1388
DB	2315	CTCTGCCCTTGATCAGCCCCCACTGGCCTAGACCCAGCAGACAGAGCAGGAGAGCTCA	2374

QY	1389	GCTGCAATCCGACGACCCCCACCCCAAGGTTCTCCAACATCACAGCCAGCCGCCCCACT	1444
DB	2375	GCTGCAATCCGACGACCCCCACCCCAAGGTTCTCCAACATCACAGCCGCCCCACT	2434
QY	1449	GGGTAATAAAAGNGGTTGTGGAAAAAAGGAAAAAAGGAAAAA	1492
DB	2435	GGGTAATAAAAGNGGTTGTGGAAAAAAGGAAAAAAGGAAAAA	2478

RESULT 12
 US-10-245-851-9
 ; Sequence 9, Application US/10245851
 ; Publication No. US20030068782A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Phillippe
 ; APPLICANT: Watanabe, Colin
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; APPLICANT: Fong, Sherman
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3630RIC93
 ; CURRENT APPLICATION NUMBER: US/10/245,851
 ; CURRENT FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: 10/197942
 ; PRIOR FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/059114
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/063046
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/065027
 ; PRIOR FILING DATE: 1997-11-10
 ; PRIOR APPLICATION NUMBER: 60/079689
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/086478
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087607
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/089801
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/090557
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090689
 ; PRIOR FILING DATE: 1998-06-25
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 116
 ; SEQ ID NO 9
 ; LENGTH: 2482
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-245-851-9

Query Match	97.5%;	Score 1468;	DB 15;	Length 2482;
Best Local Similarity	99.3%;	Pred. No. 0;		
Matches 1474;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;

QY	9	CACGAGGACGAGATCTCAAGAGTTTGGTTATGAGGCTGCTTGGGCAACAGAACAAAC	68
DB	995	CCCACGAGCAGATCTCAAGAGTTTGGTTATGAGGCTGCTTGGGCAACAGAACAAAC	1054
QY	69	TACCTTCGGGAAGAAGAGTGCAATTTAGCCTGTGCGGTGTGCAAGTGGGCTTTGAGA	128
DB	1055	TACCTTCGGGAAGAAGAGTGCAATTTAGCCTGTGCGGTGTGCAAGTGGGCTTTGAGA	1114
QY	129	GGCAGCTCTGGGGCTCAGCGACTTTCCCCAGGGCCCTCCATGGAAAGGCGGCATCCA	188

Db 1115 GGCAGCTCTGGGCTCAGGGACCTTCCGCCAGGGCCCTCCATGGAAGGGCCCATCCA 1174
Qy 189 GTGTGCTCTGGCACCTGTGAGCCACCCAGTTCCGTGAGCAATGGCTGTGATCGAC 248
Db 1175 GTGTGCTCTGGCACCTGTGAGCCACCCAGTTCCGTGAGCAATGGCTGTGATCGAC 1234
Qy 249 AGTTTCTCTGGAGTGTGACGACACCCCAACTGCCCGAGCCCTCCGACGAGGTGCTGT 308
Db 1235 AGTTTCTCTGGAGTGTGACGACACCCCAACTGCCCGAGCCCTCCGACGAGGTGCTGT 1294
Qy 309 GAAAAATACACGAGTGTGCTTTGACGAGCTCCAGCGATCCANTTCCCAGCGACAAAGGG 368
Db 1295 GAAAAATACACGAGTGTGCTTTGACGAGCTCCAGCGATCCANTTCCCAGTGACAAAGGG 1354
Qy 369 CACTGCTGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 428
Db 1355 CACTGCTGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 1414
Qy 429 AACCCCTTCAGCGAAACACTGGCCCGCTTTTACCTATGTTGTTTACGGCAACAGAAC 488
Db 1415 AACCCCTTCAGCGAAACACTGGCCCGCTTTTACCTATGTTGTTTATGGCAACAGAAC 1474
Qy 489 AACTTTGAGGAGAGCAGCAGTGCCTCGAGTCTTGTGCGGATCTCCAAAGAGGATG 548
Db 1475 AACTTTGAGGAGAGCAGCAGTGCCTCGAGTCTTGTGCGGATCTCCAAAGAGGATG 1534
Qy 549 TTTGGCCTGAGCGGGAAATCCCAATTCAGCAGCAGGCTCTGTGAGATGGCTGTGCGCA 608
Db 1535 TTTGGCCTGAGCGGGAAATCCCAATTCAGCAGCAGGCTCTGTGAGATGGCTGTGCGCA 1594
Qy 609 GTGTTCTCTGCTCATCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 668
Db 1595 GTGTTCTCTGCTCATCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1654
Qy 669 AACAGAGAAAGACTTCCAGGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 728
Db 1655 AACAGAGAAAGACTTCCAGGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1714
Qy 729 ACTGCTTCCACTACCGAGGACACGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 788
Db 1715 ACTGCTTCCACTACCGAGGACACGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1774
Qy 789 TGAGCCTGGGTCTACCGGCTCTCACTGGCCCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 848
Db 1775 TGAGCCTGGGTCTACCGGCTCTCACTGGCCCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 1834
Qy 849 TGGGCTGGGAAAACTTTGGAACAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908
Db 1835 TGGGCTGGGAAAACTTTGGAACAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1894
Qy 909 GAGACAGGGCTCCAGCCCTCTTGGAGAGTCTGAGTAACTGCTGCTGCTGCTGCTGCTGCT 968
Db 1895 GAGACAGGGCTCCAGCCCTCTTGGAGAGTCTGAGTAACTGCTGCTGCTGCTGCTGCTGCT 1954
Qy 969 TCAAAGGTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1028
Db 1955 TCAAAGGTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2014
Qy 1029 CCTGCATAGGAGTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1088
Db 2015 CCTGCATAGGAGTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2074
Qy 1089 CTACCCCATGGTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1148
Db 2075 CTACCCCATGGTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2134
Qy 1149 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCCCGAGGCTGGGAGGAGGAGGAGGAGGAG 1208
Db 2135 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCCCGAGGCTGGGAGGAGGAGGAGGAGGAG 2194
Qy 1209 GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTATTAATGCTGTGCGCATGCTGAAGAG 1268
Db 2195 GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTATTAATGCTGTGCGCATGCTGAAGAG 2254

Qy 1269 GAGGGAGAGAGGCTGTTTGGCCCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328
Db 2255 GAGGGAGAGAGGCTGTTTGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2314
Qy 1329 CTCTGCCCTTGTATCAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1388
Db 2315 CTCTGCCCTTGTATCAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2374
Qy 1389 GCTGCTATCCGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1448
Db 2375 GCTGCTATCCGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2434
Qy 1449 GGGTAATAAAAGTGGTTTGTGGAATAAAATAAAATAAAATAAAATAAAATAAA 1492
Db 2435 GGGTAATAAAAGTGGTTTGTGGAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 2478

RESULT 13
US-10-245-883-9
; Sequence 9, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C70
; CURRENT APPLICATION NUMBER: US/10/245,883
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
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; PRIOR APPLICATION NUMBER: 60/086478
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-883-9

Query Match 97.5%; Score 1468; DB 15; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 9 CACGAGGAGCAGATCTGCAAGAGTTTCTGTTTATGGAGGCTGTTGGCAACAACAAC 68

;
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/106932
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/115554
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119342
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/123957
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123972
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: 60/127372
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/131271
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/133459
; PRIOR FILING DATE: 1999-05-11
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; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 60/180921
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/187202
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/198587
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; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/206330
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/206368
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/209832
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; PRIOR FILING DATE: 2000-09-05
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; PRIOR FILING DATE: 2000-09-22
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; PRIOR APPLICATION NUMBER: 60/261910
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/261939
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/262150
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; PRIOR FILING DATE: 2001-01-25
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; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/709238
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; PRIOR APPLICATION NUMBER: 09/802706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 09/872035
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
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; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
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; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28
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; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 10/001054
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/081056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 10/119480
; PRIOR FILING DATE: 2002-04-09

Query Match 97.5%; Score 1468; DB 15; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACRAAGAAC 68
Db 995 CCCACGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACRAAGAAC 1054

QY 69 TACCTTCGGGAAGAGAGTGATTCATTTAGCCTGTGCGGGGTGTCGAAGGTGGCCCTTTGAGA 128
Db 1055 TACCTTCGGGAAGAGAGTGATTCATTTAGCCTGTGCGGGGTGTCGAAGGTGGCCCTTTGAGA 1114

QY 129 GGCAGCTCTGGGCTCAGGCGACTTTTCCCCAGGGCCCTCCAFGGAAGGCGCCATCCA 188
Db 1115 GGCAGCTCTGGGCTCAGGCGACTTTTCCCCAGGGCCCTCCAFGGAAGGCGCCATCCA 1174

QY 189 GTGTGCTCTGGCACCTGTGAGCCCAACCCAGTTCGGCTGCGATGAGTGGCTGCTGCATCGAC 248
Db 1175 GTGTGCTCTGGCACCTGTGAGCCCAACCCAGTTCGGCTGCGATGAGTGGCTGCTGCATCGAC 1234

QY 249 AGTTTCCCTGAGTGTGACGACACCCCAACTGCCCGAGCTCCCGAGGCTCCGAGGCTGCTGT 308
Db 1235 AGTTTCCCTGAGTGTGACGACACCCCAACTGCCCGAGCTCCCGAGGCTCCGAGGCTGCTGT 1294

QY 309 GAAAAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGAGCGACAAAGGS 368
Db 1295 GAAAAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGAGTGACAAAGGS 1354

QY 369 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGGATCCCGCGTGGTACTAC 428
Db 1355 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGGATCCCGCGTGGTACTAC 1414

QY 429 AACCCCTTCAGCGAAACACTGCGCCCGCTTTACCTATGTTGGTGTGTTACGGCAACAAGAC 488
Db 1415 AACCCCTTCAGCGAAACACTGCGCCCGCTTTACCTATGTTGGTGTGTTATGGCAACAAGAC 1474

QY 489 AACTTTGAGGAAGAGCAGCAGTGCTCGAGTCTTGTGCGGCGATCTCCAGAAAGGATGTG 548
Db 1475 AACTTTGAGGAAGAGCAGCAGTGCTCGAGTCTTGTGCGGCGATCTCCAGAAAGGATGTG 1534

QY 549 TTTGGCCTGAGCGGGGAAATCCCAATTCAGCAGCAGGCTCTGTGGAGATGGCTGTGCGCA 608
Db 1535 TTTGGCCTGAGCGGGGAAATCCCAATTCAGCAGCAGGCTCTGTGGAGATGGCTGTGCGCA 1594

QY 609 GTGTTCTGGTCACTGTGCAATTTGGTGGTGGTAGCCATCTTGGGTACTGCTTCTTCAAG 668
Db 1595 GTGTTCTGGTCACTGTGCAATTTGGTGGTGGTAGCCATCTTGGGTACTGCTTCTTCAAG 1654

QY 669 AACCCAGAAAGGACTTCCACGGACACCGAGCAGCTGCTTATACCAACACACCCCTGCCAGCTCC 728
Db 1655 AACCCAGAAAGGACTTCCACGGACACCGAGCAGCTGCTTATACCAACACACCCCTGCCAGCTCC 1714

QY 729 ACTGTCTCCACTACCGAGGACACCGAGCAGCTGCTTATACCAACACACCCCGGCCCTC 788
Db 1715 ACTGTCTCCACTACCGAGGACACCGAGCAGCTGCTTATACCAACACACCCCGGCCCTC 1774

QY 789 TGAGCCTGGTCTCACCGGCTCTCACCTGGCCCTGCTTCCCTGCTGCTGCAAGGAGGCGC 848
Db 1775 TGAGCCTGGTCTCACCGGCTCTCACCTGGCCCTGCTTCCCTGCTGCTGCAAGGAGGCGC 1834

QY 849 TGGGCTGGGAAAAAATTTGGAACCCAGACTCTTCCCTGTTTCCAGGCGCCACTGTGCTCA 908

RESULT 15

US-10-238-183-9

; Sequence 9, Application US/10238183

; Publication No. US20030073189A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Eaton, Dan

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Goddard, Audrey

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe

; APPLICANT: Watanabe, Colin

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; APPLICANT: Fong, Sherman

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3630R1C11

; CURRENT APPLICATION NUMBER: US/10/238,183

; CURRENT FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: 10/197942

; PRIOR FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/059114

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/063046

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/065027

; PRIOR FILING DATE: 1997-11-10

1835 TGGCTGGGAAAAAACTTTTGGAAACAGACTCTTGGCTGTTTCCAGGCCCACTGTGCTCA 1894
909 GAGACCAGGGCTCCAGCCCTCTTTGGAGAAGTCTCAGCTAAGCTCAGCTCCTGAGAAAGC 968
1895 GAGACCAGGGCTCCAGCCCTCTTTGGAGAAGTCTCAGCTAAGCTCAGCTCCTGAGAAAGC 1954
969 TCAAAAGTTTGGAAAGGAGCAGAAAAACCTTTGGGCCAGAAAGTACCAGACTAGATGGAACCTG 1028
1955 TCAAAAGTTTGGAAAGGAGCAGAAAAACCTTTGGGCCAGAAAGTACCAGACTAGATGGAACCTG 2014
1029 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1088
2015 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2074
1089 CTACCCCATGCTGTAGGAAGAGGAGTGGGTGGTGTGTCAGACCCCTGGAGGCCCAACCT 1148
2075 CTACCCCATGCTGTAGGAAGAGGAGTGGGTGGTGTGTCAGACCCCTGGAGGCCCAACCT 2134
1149 GTCTCTCCGAGCT 1208
2135 GTCTCTCCGAGCT 2194
1209 GTAGTTTGTCTGTAAAGAGTTGCTTTTGTGTTTATTAATGCTGTGGCATGGGTGAAGAG 1268
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1269 GAGGGGAAGAGGCTGTTTGGCCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328
2255 GAGGGGAAGAGGCTGTTTGGCCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2314
1329 CTCTGCCCTTGATCAGCCCAACCTGGCCTAGACAGCAGAGCCAGGAGAGCTCA 1388
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1389 GCTGCATTCGGCAGCCCAACCTGGCCTAGGTTCTTCAACATCAGCAGCCCACTGCCCCACT 1448
2375 GCTGCATTCGGCAGCCCAACCTGGCCTAGGTTCTTCAACATCAGCAGCCCACTGCCCCACT 2434
1449 GGGTAATAAAAGTGGTTGTGGAAAAAATAAAAAA 1492
2435 GGGTAATAAAAGTGGTTGTGGAAAAAATAAAAAA 2478

;
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
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; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091358
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091978
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; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/106932
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/115554
; PRIOR FILING DATE: 1999-01-12
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; PRIOR APPLICATION NUMBER: 60/144790
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145228
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146843
; PRIOR FILING DATE: 1999-08-03
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; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/177118
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; PRIOR APPLICATION NUMBER: 60/179851
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; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836
; PRIOR FILING DATE: 2001-08-16
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; PRIOR APPLICATION NUMBER: 09/946374
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; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/081056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 10/119480
; PRIOR FILING DATE: 2002-04-09

Query Match      97.5%; Score 1468; DB 15; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTATGGAGGCTGCTGGGCAACAAGAACAC 68
Db      995 CCCACGGAGCAGATCTGCAAGAGTTTCGTTATGGAGGCTGCTGGGCAACAAGAACAC 1054

QY      69 TACCTTCGGGAAGAGAGTGCAATCTAGCCTGTCCGGGTGTGCAAGTGGGCTTTGAGA 128
Db      1055 TACCTTCGGGAAGAGAGTGCAATCTAGCCTGTCCGGGTGTGCAAGTGGGCTTTGAGA 1114

QY      129 GGCAGCTCTGGGGCTCAGCGACTTTCCCCAGGGCCCTCCATGGAAAGGCCCATCCA 188
Db      1115 GGCAGCTCTGGGGCTCAGCGACTTTCCCCAGGGCCCTCCATGGAAAGGCCCATCCA 1174

QY      189 GTGTGCTCTGGCACCTGTGAGCCCAACCCAGTTCCGCTGAGCAATGGCTGTGCTATCGAC 248
Db      1175 GTGTGCTCTGGCACCTGTGAGCCCAACCCAGTTCCGCTGAGCAATGGCTGTGCTATCGAC 1234

QY      249 AGTTTCCTGGAGGTGACGACACCCCAACTGCCCGAGCCCTCCGACGAGGTGCTGT 308
Db      1235 AGTTTCCTGGAGGTGACGACACCCCAACTGCCCGAGCCCTCCGACGAGGTGCTGT 1294

QY      309 GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGAGCGACAAAGGG 368
Db      1295 GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGAGCGACAAAGGG 1354

QY      369 CACTGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 428
Db      1355 CACTGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 1414

QY      429 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTTACGSCAACAGAAC 488
Db      1415 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTTATGGCAACAGAAC 1474

QY      489 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCCGGCATCTCCAGAGAGGATGTG 548
Db      1475 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCCGGCATCTCCAGAGAGGATGTG 1534

QY      549 TTTGGCCTGAGGCGGGAATCCCAATCCAGGCTCTGTGGAGATGGCTGTCCGA 608
Db      1535 TTTGGCCTGAGGCGGGAATCCCAATCCAGGCTCTGTGGAGATGGCTGTCCGA 1594

QY      609 GTGTTCTGTCATCTGCAATGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 668
Db      609 GTGTTCTGTCATCTGCAATGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 668
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Db      1595 GTGTTCTCTGTCATCTGCAATGTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 1654
QY      669 AACGAGAGAAAGGACTTCCACGGACACCAACCAACCAACCAACCAACCAACCAACCAACCA 728
Db      1655 AACGAGAGAAAGGACTTCCACGGACACCAACCAACCAACCAACCAACCAACCAACCAACCA 1714
QY      729 ACTGTCTCTCCACTACCGAGGACACGGAGCAGCCTGGTCTATTAACCAACCAACCAACCAACCA 788
Db      1715 ACTGTCTCTCCACTACCGAGGACACGGAGCAGCCTGGTCTATTAACCAACCAACCAACCAACCA 1774
QY      789 TGAGCCTGGGCTCTACCGGCTCTCACCTGGCCCTGCTTCTCTGCTTCCCAAGGCGAGAGGCC 848
Db      1775 TGAGCCTGGGCTCTACCGGCTCTCACCTGGCCCTGCTTCTCTGCTTCCCAAGGCGAGAGGCC 1834
QY      849 TGGGCTGGGAAAAAATTTGGAACCAAGACTTTGCTTCCCTGTTTCCAGGCGCCACTGTGCTCA 908
Db      1835 TGGGCTGGGAAAAAATTTGGAACCAAGACTTTGCTTCCCTGTTTCCAGGCGCCACTGTGCTCA 1894
QY      909 GAGACCAAGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGCTCCTGAGAAAGC 968
Db      1895 GAGACCAAGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGCTCCTGAGAAAGC 1954
QY      969 TCAAAGGTTTGGAAAGGAGCAGAAACCTTGGGGCCAGAGTACCAGACTAGTAGGACCTG 1028
Db      1955 TCAAAGGTTTGGAAAGGAGCAGAAACCTTGGGGCCAGAGTACCAGACTAGTAGGACCTG 2014
QY      1029 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTTTCAAAGCTGCTGTCC 1088
Db      2015 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTTTCAAAGCTGCTGTCC 2074
QY      1089 CTACCCCATGGTCTAGGAAGAGAGTGGGGTGGTGTGAGACCTTGGAGGCCCAACCCCT 1148
Db      2075 CTACCCCATGGTCTAGGAAGAGAGTGGGGTGGTGTGAGACCTTGGAGGCCCAACCCCT 2134
QY      1149 GTCTCTCCGAGCTCCTCTTCCATGCTGTGCGCCAGGGCTGGGAGGAAGACTTCCCTGT 1208
Db      2135 GTCTCTCCGAGCTCCTCTTCCATGCTGTGCGCCAGGGCTGGGAGGAAGACTTCCCTGT 2194
QY      1209 GTAGTTTGTGCTGTAAGAGTGTGCTTTTGTATTATTAATGCTGTGGCATGGGTGAAGAG 1268
Db      2195 GTAGTTTGTGCTGTAAGAGTGTGCTTTTGTATTATTAATGCTGTGGCATGGGTGAAGAG 2254
QY      1269 GAGGGGAAGAGGCTGTTTGGCCCTCTCTATCCTCTCTTCTCTTCCCAAGATTGAGCT 1328
Db      2255 GAGGGGAAGAGGCTGTTTGGCCCTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2314
QY      1329 CTCTGCCCTTGATCAGCCCAACCCCTGGCTTAGACCCAGCAGACAGAGCCAGGAGAGCTCA 1388
Db      2315 CTCTGCCCTTGATCAGCCCAACCCCTGGCTTAGACCCAGCAGACAGAGCCAGGAGAGCTCA 2374
QY      1389 GCTGCATTCGCGAGCCCAACCCCAAGGTTCTCCAACATCAGCCAGCCCGCCCACT 1448
Db      2375 GCTGCATTCGCGAGCCCAACCCCAAGGTTCTCCAACATCAGCCAGCCCGCCCACT 2434
QY      1449 GGGTAATAAAGTGGTTTGTGGAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1492
Db      2435 GGGTAATAAAGTGGTTTGTGGAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2478
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Search completed: April 22, 2004, 08:23:12
Job time : 663 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2004, 00:39:17 ; Search time 636 Seconds
(without alignments)
10052.733 Million cell updates/sec

Title: US-09-935-390A-4
Perfect score: 1505
Sequence: 1 GAATTGGCAGCAGGAGCAG.....AAAAAAGTCTGCGGCGC 1505

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002s.*
7: geneseqn2003as.*
8: geneseqn2003bs.*
9: geneseqn2003cs.*
10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1505	100.0	1505	2	AAV43604	Aav43604 Human sec
2	1468	97.5	2482	4	AAF30055	Aaf30055 Human CDN
3	1468	97.5	2482	4	AAD16721	Aad16721 Human hep
4	1468	97.5	2482	6	ABK40259	Abk40259 cDNA enco
5	1468	97.5	2482	6	ABL88092	Ab188092 Human PRO
6	1468	97.5	2482	6	ABK69965	Abk69965 cDNA enco
7	1468	97.5	2482	6	ABL95581	Ab195581 Human ang
8	1468	97.5	2482	8	ADA01277	Ada01277 Human PRO
9	1468	97.5	2482	8	ADA43706	Ada43706 Human CDN
10	1468	97.5	2482	8	ADA43474	Ada43474 Human CDN
11	1468	97.5	2482	8	ADA01149	Ada01149 Human PRO
12	1468	97.5	2482	8	ADA01033	Ada01033 Human CDN
13	1468	97.5	2482	8	ADA43590	Ada43590 Human CDN
14	1468	97.5	2482	8	ADA06852	Ada06852 Human PRO
15	1468	97.5	2482	8	ADA08340	Ada08340 Novel hum
16	1468	97.5	2482	8	ADB99633	Adb99633 Human PRO
17	1468	97.5	2482	8	ADB86916	Adb86916 Human PRO
18	1468	97.5	2482	8	ADB66071	Adb66071 Human CDN
19	1468	97.5	2482	9	ADB99749	Adb99749 Human PRO
20	1468	97.5	2482	9	ADB99404	Adb99404 Novel hum
21	1468	97.5	2482	9	ADB65955	Adb65955 Human CDN
22	1468	97.5	2482	9	ADC23353	Adc23353 Human CDN
23	1468	97.5	2482	9	ADC26046	Adc26046 Human PRO

24	1468	97.5	2482	9	ADD10330	Add10330 Human sec
25	1468	97.5	2482	9	ADD11290	Add11290 Human sec
26	1468	97.5	2482	9	ADD37083	Add37083 Human sec
27	1468	97.5	2482	9	ADE04873	Ade04873 Human PRO
28	1468	97.5	2482	9	ADE11179	Ade11179 Human PRO
29	1468	97.5	2482	9	ADD88110	Add88110 Human PRO
30	1468	97.5	2482	9	ADD95405	Add95405 Human CDN
31	1468	97.5	2482	9	ADE06335	Ade06335 Human PRO
32	1468	97.5	2482	9	ADE38110	Ade38110 Human PRO
33	1468	97.5	2482	9	ADD88226	Add88226 Human PRO
34	1468	97.5	2482	9	ADD90807	Add90807 Human CDN
35	1468	97.5	2482	10	ADE51660	Ade51660 Human CDN
36	1468	97.5	2482	10	ADE51776	Ade51776 Human CDN
37	1468	97.5	2482	10	ADE37634	Ade37634 Human CDN
38	1468	97.5	2482	10	ADE37518	Ade37518 Human CDN
39	1468	97.5	2482	10	ADD95289	Add95289 Human CDN
40	1468	97.5	2482	10	ADE37989	Ade37989 Human PRO
41	1468	97.5	2482	10	ADE76078	Ade76078 Human PRO
42	1468	97.5	2482	10	ADE39401	Ade39401 Human PRO
43	1468	97.5	2482	10	ADE04205	Ade04205 Human PRO
44	1468	97.5	2482	10	ADE39802	Ade39802 Human PRO
45	1468	97.5	2482	10	ADE19667	Ade19667 Human PRO

ALIGNMENTS

RESULT 1
AAV43604
ID AAV43604 standard; DNA; 1505 BP.
XX
AC AAV43604;
XX
DT 24-SEP-1998 (first entry)
XX
DE Human secreted protein 4 encoding DNA.
XX
KW Secreted protein; human; cell proliferation; cytokine activity;
tissue growth; cellular differentiation; regeneration; activin; inhibin;
chemotactic; haemostatic; thrombolytic; tumour inhibition;
anti-inflammatory activity; biomarker; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 171..791
FT /*tag= a
FT /product= "human secreted protein"
XX
PN WO9825959-A2.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US022787.
XX
PR 11-DEC-1996; 96US-0032757P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Escobedo J, Hu Q, Garcia P, Williams LT, Kothakota S;
XX
DR WPI; 1998-348453/30.
DR P-PSDB; AAW63684.
XX
PT Secreted human polypeptides - having cytokine, cell proliferation or
differentiation, activin or inhibin, tumour inhibition or anti-
inflammatory activities.
XX
PS Claim 6; Page 31-32; 78pp; English.
XX
CC This DNA encodes a human secreted protein. The specification provides
secreted protein sequences (AAW63681 to AAW63699) encoded by the nucleic
acid sequences shown in AAV43601 to AAV43619. The invention provides a

CC method of identifying a secreted polypeptide which is modified by rough
CC microsomes. The secreted proteins can be used in assays to determine
CC biological activities, such as cytokine, cell proliferation, or cellular
CC differentiation activities, tissue growth or regeneration, activin or
CC inhibin activity, chemotactic or chemokinetic activity, haemostatic or
CC thrombolytic activity, receptor/ligand activity, tumour inhibition, or
CC anti-inflammatory activity. The proteins can also be used as biomarkers,
CC to identify tissues or cell types which express the proteins, or a stage-
CC or disease-specific alteration in protein expression. They can be used in
CC protein interaction assays, to identify ligands or binding proteins
CC Compounds which affect the biological activities of the secreted proteins
CC or their ability to interact with specific ligands can be identified
CC using the proteins in screening assays. The proteins and antibodies that
CC bind specifically to the protein can also be used to design diagnostic
CC tests and therapeutic compositions for diseases which may be associated
CC with altered expression of these proteins. Fusion proteins comprising,
CC e.g. signal sequences or transmembrane domains of the proteins can be
CC used to target other protein domains to cellular membrane or they can be
CC secreted extracellularly
XX

SQ Sequence 1505 BP; 332 A; 450 C; 406 G; 317 T; 0 U; 0 Other;

Query Match 100.0%; Score 1505; DB 2; Length 1505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATTCGGCACGAGGAGCAGATCTGCAAGAGTTTCGTTATGAGGCTGCTGGGCAACA	60
Db	1	GAATTCGGCACGAGGAGCAGATCTGCAAGAGTTTCGTTATGAGGCTGCTGGGCAACA	60
Qy	61	AGAACAACTACCTTCGGGAAGAGAGTGTAGCTGTGCGGGTGTGCAAGTGGG	120
Db	61	AGAACAACTACCTTCGGGAAGAGAGTGTAGCTGTGCGGGTGTGCAAGTGGG	120
Qy	121	CTTTGAGAGGCGAGCTCTGGGCTCAGGCGACTTTCCTCCAGGGCCCTCCATGGAAGGC	180
Db	121	CTTTGAGAGGCGAGCTCTGGGCTCAGGCGACTTTCCTCCAGGGCCCTCCATGGAAGGC	180
Qy	181	GCCATCCAGTGTGCTCTGGCACCTGTGACGCCACCCAGTTCCGCTGCAAGTGGCTGCT	240
Db	181	GCCATCCAGTGTGCTCTGGCACCTGTGACGCCACCCAGTTCCGCTGCAAGTGGCTGCT	240
Qy	241	GCATCGACAGTTTCCTGGAGTGTGACGACACCCCGAATGCTCCCGACGAGG	300
Db	241	GCATCGACAGTTTCCTGGAGTGTGACGACACCCCGAATGCTCCCGACGAGG	300
Qy	301	CTGCTGTGAAATAATACAGAGTGGCTTTGACGAGCTCCAGGCGATCCATTTCCCGAGCG	360
Db	301	CTGCTGTGAAATAATACAGAGTGGCTTTGACGAGCTCCAGGCGATCCATTTCCCGAGCG	360
Qy	361	ACAAAGGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCT	420
Db	361	ACAAAGGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCT	420
Qy	421	GGTACTACAAACCCCTTCAGGAACTGCGCCCGCTTTACCTATGTTGGTTACGGCA	480
Db	421	GGTACTACAAACCCCTTCAGGAACTGCGCCCGCTTTACCTATGTTGGTTACGGCA	480
Qy	481	ACAAGAACAACTTTGAGGAGAGCAGCAGTGCCCTCGAGTCTTCTCGCGGCACTTCCAAGA	540
Db	481	ACAAGAACAACTTTGAGGAGAGCAGCAGTGCCCTCGAGTCTTCTCGCGGCACTTCCAAGA	540
Qy	541	AGGATGTGTTGGCTTGAGGCGGGAATATCCCATTTCCAGCAGCAGGCTCTGTGGAGATGG	600
Db	541	AGGATGTGTTGGCTTGAGGCGGGAATATCCCATTTCCAGCAGCAGGCTCTGTGGAGATGG	600
Qy	601	CTGTCGAGTGTTCCTGGTCACTTGTGATGTTGGTGGTAGCCATCTTGGGTTACTGCT	660
Db	601	CTGTCGAGTGTTCCTGGTCACTTGTGATGTTGGTGGTAGCCATCTTGGGTTACTGCT	660
Qy	661	TCTTCAAGAACAGAGAAAGGACTTCCACGGACACCCACCCACCCACCCCTG	720
Db	661	TCTTCAAGAACAGAGAAAGGACTTCCACGGACACCCACCCACCCACCCCTG	720

Qy	721	CCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCAACACCGC	780
Db	721	CCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCAACACCGC	780
Qy	781	GGCCCTCTGAGCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTGCTTCCCAAGG	840
Db	781	GGCCCTCTGAGCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTGCTTCCCAAGG	840
Qy	841	CAGAGGCTGGCTGGGAAACCTTTGGAAACAGACTCTTGCTGCTTCCAGGCCCCACT	900
Db	841	CAGAGGCTGGCTGGGAAACCTTTGGAAACAGACTCTTGCTGCTTCCAGGCCCCACT	900
Qy	901	GTGCTCAGAGACCAAGGCTCCAGCCCTCTTGAGAAAGTCTCAGCTAAGCTCAGTCTCT	960
Db	901	GTGCTCAGAGACCAAGGCTCCAGCCCTCTTGAGAAAGTCTCAGCTAAGCTCAGTCTCT	960
Qy	961	GAGAAAGCTCAAAGGTTTGAAGGAGCAGAAACCTTTGGGCCAGAAAGTACAGACTAGA	1020
Db	961	GAGAAAGCTCAAAGGTTTGAAGGAGCAGAAACCTTTGGGCCAGAAAGTACAGACTAGA	1020
Qy	1021	TGGACCTGCCTGATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTTCAAAGCT	1080
Db	1021	TGGACCTGCCTGATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTTCAAAGCT	1080
Qy	1081	GCCTGTCCCTACCCCATGGTCTAGGAAGAGGAGTGGGTGGTGTGAGACCTTGAGGCCC	1140
Db	1081	GCCTGTCCCTACCCCATGGTCTAGGAAGAGGAGTGGGTGGTGTGAGACCTTGAGGCCC	1140
Qy	1141	CCAAACCTGTCTCCCGAGCTCTCTTCCATGCTGTCGCCCGAGGGCTGGGAGGAGGAC	1200
Db	1141	CCAAACCTGTCTCCCGAGCTCTCTTCCATGCTGTCGCCCGAGGGCTGGGAGGAGGAC	1200
Qy	1201	TTCCCTGTGTAGTTTGTGCTGTAAAGAGTTGCTTTTGTATTATTTAATGCTGTGGCATGG	1260
Db	1201	TTCCCTGTGTAGTTTGTGCTGTAAAGAGTTGCTTTTGTATTATTTAATGCTGTGGCATGG	1260
Qy	1261	GTGAAGAGGAGGGGAAGAGGCTGTTTGGGCTCTCTATCTCTCTTCTTCCCCCAAG	1320
Db	1261	GTGAAGAGGAGGGGAAGAGGCTGTTTGGGCTCTCTATCTCTCTTCTTCCCCCAAG	1320
Qy	1321	ATTGAGCTCTTGCCCTTGATCAGCCCCCACCCTGGGCTAGACAGCAGAGCCAGGA	1380
Db	1321	ATTGAGCTCTTGCCCTTGATCAGCCCCCACCCTGGGCTAGACAGCAGAGCCAGGA	1380
Qy	1381	GAAGCTCAGCTGCATTCCGAGCCCCCACCCTGGGCTAGACAGCAGAGCCAGCC	1440
Db	1381	GAAGCTCAGCTGCATTCCGAGCCCCCACCCTGGGCTAGACAGCAGAGCCAGCC	1440
Qy	1441	CGCCCACTGGGTAATAAAGTGGTTGTGAAAAAATAAATAAATAAATAAATAAATAAATAA	1500
Db	1441	CGCCCACTGGGTAATAAAGTGGTTGTGAAAAAATAAATAAATAAATAAATAAATAAATAA	1500
Qy	1501	GCCGC 1505	
Db	1501	GCCGC 1505	

RESULT 2
AAF30055
ID AAF30055 standard; cDNA; 2482 BP.

XX AAF30055;

XX 30-APR-2001 (first entry)

XX Human cDNA encoding PRO256.

PRO256; UNQ223; human; immune disease; autoimmune disease; antirheumatic;
antiarthritic; antiinflammatory; antianaemic; immunosuppressive;
antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide;
dermatological; antipsoriatic; antiasthmatic; antiallergic;
immunostimulant; protease inhibitor; ss.

Db 2015 CCTGCATAGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTCTCAAAAGCTGCCTGTCC 2074
QY 1089 CTACCCCATGGTCTAGGAAGAGAGAGTGGGGTGGTGTGACAGCCTGGAGGCCCAACCCCT 1148
Db 2075 CTACCCCATGGTCTAGGAAGAGAGTGGGGTGGTGTGACAGCCTGGAGGCCCAACCCCT 2134
QY 1149 GTCCTCCGAGCTCCTCTTCCATGCTGTGCGGCCAGGGCTGGAGGAAGCACTTCCCTGT 1208
Db 2135 GTCCTCCGAGCTCCTCTTCCATGCTGTGCGGCCAGGGCTGGAGGAAGCACTTCCCTGT 2194
QY 1209 GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTATTATTAATGCTGTGGCATGGTGAAGAG 1268
Db 2195 GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTATTATTAATGCTGTGGCATGGTGAAGAG 2254
QY 1269 GAGGGGAAGAGGCTGTTTGGCCCTCTCTATCCTCTCTTCTTCTTCTTCTTCTTCTTCT 1328
Db 2255 GAGGGGAAGAGGCTGTTTGGCCCTCTCTATCCTCTCTTCTTCTTCTTCTTCTTCTTCT 2314
QY 1329 CTCTGCCCTTATCAGCCCCACCCCTGGCTAGACCAGCAGACAGAGCCAGGAGGCTCA 1388
Db 2315 CTCTGCCCTTATCAGCCCCACCCCTGGCTAGACCAGCAGACAGAGCCAGGAGGCTCA 2374
QY 1389 GCTGCTATCCGAGCCCCACCCCTGGCTAGACCAGCAGACAGAGCCAGGAGGCTCA 1448
Db 2375 GCTGCTATCCGAGCCCCACCCCTGGCTAGACCAGCAGACAGAGCCAGGAGGCTCA 2434
QY 1449 GGGTAATAAAGTGGTTTGTGGAAAAAAGGTTCTCCAAATCATCAGAGCCAGCCCACT 1492
Db 2435 GGGTAATAAAGTGGTTTGTGGAAAAAAGGTTCTCCAAATCATCAGAGCCAGCCCACT 2478

RESULT 3

ID AAD16721 standard; cDNA; 2482 BP.

XX AAD16721;

DT 19-NOV-2001 (first entry)

XX Human hepatocyte growth factor activator inhibitor, PRO256 cDNA.

KW Human; PRO256 protein; cardiovascular; endothelial; angiogenic disorder;
cardiac hypertrophy; trauma; cardiac; age-related macular degeneration;
gene therapy; angiogenesis; protease activity; hepatocyte growth factor;
peripheral vascular disease; hepatic; renal injury; nephrotropic; tumour;
restinosis; tranquilizer; vulnery; cytosolic; hepatotropic; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FH 188..1777

FT CDS /*tag= a
FT /product= "Human hepatocyte growth factor activator
inhibitor, PRO256"

FT sig_peptide 188..292

FT mat_peptide 293..1774

FT /*tag= c
FT /product= "Human mature hepatocyte growth factor
activator inhibitor, PRO256"

XX WO200159100-A2.

XX 16-AUG-2001.

XX 19-DEC-2000; 2000WO-US034756.

XX 11-FEB-2000; 2000WO-US003565.

XX 15-MAR-2000; 2000WO-US006884.

XX 28-NOV-2000; 2000US-0253665P.

XX (GETH) GENENTECH INC.

PI Gurney AL, Kirchhofer DK, Wood WI;

XX WPI; 2001-541567/60.

DR P-PSDB; AAE09332.

XX An isolated polypeptide designated PRO256 useful for treating a
cardiovascular, endothelial, or angiogenic disorder.

PT Claim 40; Fig 1; 124pp; English.

XX The present invention relates to PRO256 or its agonist/antagonist may be
used to treat a cardiovascular, endothelial, or angiogenic disorder in a
mammal, especially a human with cardiac hypertrophy, trauma, a type of
tumour or age-related macular degeneration. PRO256 may be administered
together with a cardiovascular, endothelial, or angiogenic agent, a
chemotherapeutic agent, a growth inhibitory agent, or a cytotoxic agent.
PRO256 may also be used to treat the disorders above, preferably through
administration via ex vivo gene therapy. PRO256 or its agonist may be
used to inhibit endothelial cell growth, angiogenesis or protease
activity of a hepatocyte growth factor, whereas an antagonist of PRO256
may be used to stimulate endothelial cell growth, angiogenesis or
protease activity of a hepatocyte growth factor. Stimulation or
inhibition of the protease activity of a hepatocyte growth factor is
preferably carried out where a mammal has a cardiovascular, endothelial,
or angiogenic disorder selected from peripheral vascular disease, hepatic
or renal injury or a restinosis disorder. The present sequence is human
hepatocyte growth factor activator inhibitor, PRO256 cDNA

XX Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Query Match 97.5%; Score 1468; DB 4; Length 2482;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 9 CACGAGGAGCAGATCTCAAGAGTTTCGTTTATGAGGCTGCTTGGCAACAAGAACAC 68

Db 995 CCCACGGAGCAGATCTCAAGAGTTTCGTTTATGAGGCTGCTTGGCAACAAGAACAC 1054

QY 69 TACCTTCGGGAAGAGAGTGCATTTAGCCTGTGCGGGTGTGCAAGGTGGGCTTTGAGA 128

Db 1055 TACCTTCGGGAAGAGAGTGCATTTAGCCTGTGCGGGTGTGCAAGGTGGGCTTTGAGA 1114

QY 129 GGCAGCTCTGGGCTCAGCGGACCTTCCGCCAGGGCCCTCCATGGAAGGGCCATCCA 188

Db 1115 GGCAGCTCTGGGCTCAGCGGACCTTCCGCCAGGGCCCTCCATGGAAGGGCCATCCA 1174

QY 189 GTGTGCTCTGGCACCTGTGAGCCACCCAGTTCGCTGCAGCAATGGCTGCTGCATCGAC 248

Db 1175 GTGTGCTCTGGCACCTGTGAGCCACCCAGTTCGCTGCAGCAATGGCTGCTGCATCGAC 1234

QY 249 AGTTTCTCTGGAGTGTGACGACACCCGCCAAGTCCCGACGCGCTCCGACGAGCTGCTGT 308

Db 1235 AGTTTCTCTGGAGTGTGACGACACCCGCCAAGTCCCGACGCGCTCCGACGAGCTGCTGT 1294

QY 309 GAAAAATACACGAGTGGCTTTGACGAGCTCCAGGCTCCATTTCCCGCGGACAAAGGG 368

Db 1295 GAAAAATACACGAGTGGCTTTGACGAGCTCCAGGCTCCATTTCCCGCGGACAAAGGG 1354

QY 369 CACTGCGTGGACCTGCGGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 428

Db 1355 CACTGCGTGGACCTGCGGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 1414

QY 429 AACCCCTTCAGCGAACACTGCGGCCGCTTTTACCTATGTTGTTTACGCAACAAGAAC 488

Db 1415 AACCCCTTCAGCGAACACTGCGGCCGCTTTTACCTATGTTGTTTACGCAACAAGAAC 1474

QY 489 AACTTTGAGGAAGAGCAGTGCCTCGAGTCTTGTGCGGCAATCTCCAGAGGATGTG 548

Db 1475 AACTTTGAGGAAGAGCAGTGCCTCGAGTCTTGTGCGGCAATCTCCAGAGGATGTG 1534

QY 549 TTTGGCCTGAGGCGGGAATCCCAATTCAGCAGGCTCTGTGGAGATGGCTGTGCA 608

Db 1535 TTTGGCCTGAGGCGGGAATCCCAATTCAGCAGGCTCTGTGGAGATGGCTGTGCA 1594

QY 609 GTGTTCTGGTCACTGATGTTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 668
DB 1595 GTGTTCTGGTCACTGATGTTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 1654
QY 669 AACCAGAGAAAGGACTTCCACGGACACACACACACACACACACACACACACACACACAC 728
DB 1655 AACCAGAGAAAGGACTTCCACGGACACACACACACACACACACACACACACACACACAC 1714
QY 729 ACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATATAACACACACACACACAC 788
DB 1715 ACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATATAACACACACACACACAC 1774
QY 789 TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTCTGCTTGGCCAAAGCAGAGCC 848
DB 1775 TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTCTGCTTGGCCAAAGCAGAGCC 1834
QY 849 TGGGCTGGGAAAAAATTGGAAACAGACTCTTGGCTGTTTCCAGGCCACCTGTCCTCA 908
DB 1835 TGGGCTGGGAAAAAATTGGAAACAGACTCTTGGCTGTTTCCAGGCCACCTGTCCTCA 1894
QY 909 GAGACACAGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCACGCTCTGAGAAAGC 968
DB 1895 GAGACACAGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCACGCTCTGAGAAAGC 1954
QY 969 TCAAAGGTTTGGAGAGGAGAGAAAAACCTTGGGCCAGAGTACCAGACTAGATGACCTG 1028
DB 1955 TCAAAGGTTTGGAGAGGAGAGAAAAACCTTGGGCCAGAGTACCAGACTAGATGACCTG 2014
QY 1029 CCTGCATAGGAGTTTGGAGAGTGGAGTTTGTGTTTCTCTGTTTCAAAGCTGCTGTC 1088
DB 2015 CCTGCATAGGAGTTTGGAGAGTGGAGTTTGTGTTTCTCTGTTTCAAAGCTGCTGTC 2074
QY 1089 CTACCCCATGGTCTAGGAGAGGAGTGGGTTGGTGTGAGACCTTGGAGGCCCAACCCCT 1148
DB 2075 CTACCCCATGGTCTAGGAGAGGAGTGGGTTGGTGTGAGACCTTGGAGGCCCAACCCCT 2134
QY 1149 GTCTCTCCGAGCTCCTCTTCCATGCTGTGGCCCGAGGCTGGGAGGAGGAGCTTCCCTGT 1208
DB 2135 GTCTCTCCGAGCTCCTCTTCCATGCTGTGGCCCGAGGCTGGGAGGAGGAGCTTCCCTGT 2194
QY 1209 GTAGTTGTGCTGTAAAGAGTTGCTTTTGTGTTTATTAATGCTGTGGCATGGTGAAGAG 1268
DB 2195 GTAGTTGTGCTGTAAAGAGTTGCTTTTGTGTTTATTAATGCTGTGGCATGGTGAAGAG 2254
QY 1269 GAGGGGAAGAGGCTGTTGGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328
DB 2255 GAGGGGAAGAGGCTGTTGGCT 2314
QY 1329 CTCTGCCCTTGATCAGCCCTGAGGCTGAGCCAGCAGACAGAGCCAGGAGAGCTCA 1388
DB 2315 CTCTGCCCTTGATCAGCCCTGAGGCTGAGCCAGCAGACAGAGCCAGGAGAGGCTCA 2374
QY 1389 GCTGCATTCGCGAGCCCTGAGGCTTCTCCAACTCAGAGCCAGCCGCTGCTCACT 1448
DB 2375 GCTGCATTCGCGAGCCCTGAGGCTTCTCCAACTCAGAGCCAGCCGCTGCTCACT 2434
QY 1449 GGGTAATAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1492
DB 2435 GGGTAATAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2478

RESULT 4
ID ABK40259 standard; cDNA; 2482 BP.
XX
AC ABK40259;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human PRO256 polypeptide.
XX
KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;

KW leukaemia; neuronal disorder; stromal disorder; blastocoeleic disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytostatic; neuroprotective; gene; ss.
XX Homo sapiens.
OS
XX WO200153486-A1.
PN
XX
XX
PD 26-JUL-2001.
XX
XX 11-FEB-2000; 2000WO-US003565.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 11-MAR-1999; 99US-0123972P.
PR 11-MAY-1999; 99US-0133459P.
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 22-JUN-1999; 99US-0140653P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149395P.
PR 31-AUG-1999; 99US-0151689P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 05-JAN-2000; 2000WO-US000219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX
DR WFI; 2002-205567/26.
DR P-PSDB; AAU86133.
XX
PT Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.
XX
PS Claim 50; Fig 11; 302pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The PRO
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
CC treating benign or malignant tumours (e.g. renal, kidney, bladder,
CC breast, etc), leukaemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC stromal and blastocoeleic disorders, inflammatory, immune and angiogenic
CC disorders. The polynucleotide sequences are also useful in gene therapy.
CC ABK40254-ABK40288 encode for the human PRO polypeptides of the invention
XX
SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Query Match 97.5%; Score 1468; DB 6; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGTTGGGCAACAAGAACAC 68
DB 995 CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGTTGGGCAACAAGAACAC 1054
QY 69 TACCTTCGGGAAGAAGAGTGCATTCAGCCTGTGGGGTGTGCAAGTGGGCTTTGAGA 128
DB 1055 TACCTTCGGGAAGAAGAGTGCATTCAGCCTGTGGGGTGTGCAAGTGGGCTTTGAGA 1114
QY 129 GGCAGCTCTGGGGCTCAGGCGACTTTCCCGCCAGGCGCCCTCCATGGAAGGCGCCATCCA 188
DB 1115 GGCAGCTCTGGGGCTCAGGCGACTTTCCCGCCAGGCGCCCTCCATGGAAGGCGCCATCCA 1174

PR 25-MAY-2001; 2001US-00856034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX (GETH) GENENTECH INC.
PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-090516/12.
DR P-PSDB; ABB84837.
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
PT Claim 2; Fig 41; 565pp; English.
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic, antiangiogenic, hypotensive, vulnery and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention
XX Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
SQ Query Match 97.5%; Score 1468; DB 6; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGAGGCTGCTGGGCAACAACAAC 68
Db 995 CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGAGGCTGCTGGGCAACAACAAC 1054
QY 69 TACCTTCGGGAAGAGAGTGCTTCTAGCCTGTGCGGGTGTGCAAGTGGGCTTTGAGA 128
Db 1055 TACCTTCGGGAAGAGAGTGCTTCTAGCCTGTGCGGGTGTGCAAGTGGGCTTTGAGA 1114
QY 129 GGCAGCTCTGGGGCTCAGCGGACTTTCGCCAGGCCCCCTCCATGGAAGCGCCATCCA 188
Db 1115 GGCAGCTCTGGGGCTCAGCGGACTTTCGCCAGGCCCCCTCCATGGAAGCGCCATCCA 1174
QY 189 GTGTGCTCTGGCACCTGTGAGCCACCCAGTTCGCTGCGAGCAATGGCTGCTGCATCGAC 248
Db 1175 GTGTGCTCTGGCACCTGTGAGCCACCCAGTTCGCTGCGAGCAATGGCTGCTGCATCGAC 1234
QY 249 AGTTTCCTGGAGTGTGACGACACCCCAACTGCCCGAGCGCTCCGACGAGCTGCCTGT 308
Db 1235 AGTTTCCTGGAGTGTGACGACACCCCAACTGCCCGAGCGCTCCGACGAGCTGCCTGT 1294
QY 309 GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGCAGCAAGGG 368
Db 1295 GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGCAGCAAGGG 1354
QY 369 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 428
Db 1355 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 1414
QY 429 AACCCCTTCAGCGAACACTGCGCCCGCTTTTACCTATGCTGGTGTGTTACGCAACAAGAAC 488
Db 1415 AACCCCTTCAGCGAACACTGCGCCCGCTTTTACCTATGCTGGTGTGTTATGCAACAAGAAC 1474

QY 489 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGGCATCTCCAAGAAGGATGTG 548
Db 1475 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGGCATCTCCAAGAAGGATGTG 1534
QY 549 TTTGGCCTGAGGGCGGAAATCCCATTTCCAGCACAGGCTCTGTGGAGATGGCTGTGCA 608
Db 1535 TTTGGCCTGAGGGCGGAAATCCCATTTCCAGCACAGGCTCTGTGGAGATGGCTGTGCA 1594
QY 609 GTGTTCTGCTCATCTGCATTGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 668
Db 1595 GTGTTCTGCTCATCTGCATTGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 1654
QY 669 AACCCAGAGAAAGGACTTCCACGAGACACACACACACACACACACACACACACACCTCC 728
Db 1655 AACCCAGAGAAAGGACTTCCACGAGACACACACACACACACACACACACACACACCTCC 1714
QY 729 ACTGTCTCCACTACCGAGGACACGAGGACCTGGTCTATTAACACACACACACACACCTC 788
Db 1715 ACTGTCTCCACTACCGAGGACACGAGGACCTGGTCTATTAACACACACACACACCTC 1774
QY 789 TGAGCCTGGGCTCTCACCGGCTCTCACCTGGCCCTGCTTCTCTGTTGCCAAGGAGGCTC 848
Db 1775 TGAGCCTGGGCTCTCACCGGCTCTCACCTGGCCCTGCTTCTCTGTTGCCAAGGAGGCTC 1834
QY 849 TGGGCTGGGAAAAAATTTGGAAACAGACTCTTGCCTGTTTCCAGGCCCCACTGTGCCTCA 908
Db 1835 TGGGCTGGGAAAAAATTTGGAAACAGACTCTTGCCTGTTTCCAGGCCCCACTGTGCCTCA 1894
QY 909 GAGACCAAGGCTCCAGCCCTCTTGGAGAAAGTCTCAGCTAAGCTCAGTCTCAGAAAGC 968
Db 1895 GAGACCAAGGCTCCAGCCCTCTTGGAGAAAGTCTCAGCTAAGCTCAGTCTCAGAAAGC 1954
QY 969 TCAAAGGTTTGGAGGAGCAGAAACCTTGGGCCAGAGTACAGACTAGATGACCTG 1028
Db 1955 TCAAAGGTTTGGAGGAGCAGAAACCTTGGGCCAGAGTACAGACTAGATGACCTG 2014
QY 1029 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTTCAAAGCTGCTGTCC 1088
Db 2015 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTTCAAAGCTGCTGTCC 2074
QY 1089 CTACCCCATGGTGTAGGAAGAGGAGTGGGTGGTGTGAGCCCTGGAGGCCCCAACCT 1148
Db 2075 CTACCCCATGGTGTAGGAAGAGGAGTGGGTGGTGTGAGCCCTGGAGGCCCCAACCT 2134
QY 1149 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCCAGGGCTGGGAGGAAGGACTTCCCTGT 1208
Db 2135 GTCTCTCCGAGCTCTCTTCCATGCTGTGCGCCAGGGCTGGGAGGAAGGACTTCCCTGT 2194
QY 1209 GTAGTTTGTGCTGTAAGAGTGTCTTTTGTATTTATTTATGCTGTGGCATGGGTGAAGAG 1268
Db 2195 GTAGTTTGTGCTGTAAGAGTGTCTTTTGTATTTATTTATGCTGTGGCATGGGTGAAGAG 2254
QY 1269 GAGGGAAGAGGCTGTGTTGGCCCTCTATCCTCTCTTCTCTTCCCCCAAGATTGAGCT 1328
Db 2255 GAGGGAAGAGGCTGTGTTGGCCCTCTCTGTCTCTCTTCCCCCAAGATTGAGCT 2314
QY 1329 CTCTGCCCTTGATCAGCCCCACCTGGCCCTAGACCAAGAGACAGAGCCAGGAGGCTCA 1388
Db 2315 CTCTGCCCTTGATCAGCCCCACCTGGCCCTAGACCAAGAGACAGAGCCAGGAGGCTCA 2374
QY 1389 GCTGATTCGCGAGCCCCACCCCAAGGTTCTCCAACATCAGCCCCAGCCCCGCTACT 1448
Db 2375 GCTGATTCGCGAGCCCCACCCCAAGGTTCTCCAACATCAGCCCCAGCCCCGCTACT 2434
QY 1449 GGGTAATAAAGTGGTTTGTGGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 1492
Db 2435 GGGTAATAAAGTGGTTTGTGGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 2478

RESULT 6
ABK69965
ID ABK69965 standard; DNA; 2482 BP.

XX ABK69965;
 AC
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE cDNA encoding human Pro peptide #5.
 XX
 KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
 KW genetic disorder; tumour; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200224888-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 29-AUG-2001; 2001WO-US027099.
 XX
 PR 01-SEP-2000; 2000US-0229896P.
 PR 05-SEP-2000; 2000US-0230621P.
 PR 22-SEP-2000; 2000US-0235147P.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 12-JAN-2001; 2001US-0261878P.
 PR 16-JAN-2001; 2001US-0261910P.
 PR 16-JAN-2001; 2001US-0261939P.
 PR 16-JAN-2001; 2001US-0262150P.
 PR 25-JAN-2001; 2001US-0264395P.
 PR 02-FEB-2001; 2001US-0266421P.
 PR 09-FEB-2001; 2001US-0267623P.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001US-0274399P.
 PR 03-APR-2001; 2001US-0280382P.
 PR 04-APR-2001; 2001US-0282129P.
 PR 04-APR-2001; 2001US-0282199P.
 PR 09-MAY-2001; 2001US-0290589P.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX
 DR WPI; 2002-362426/39.
 DR P-PSDB; ABG34034.
 XX
 PT New PRO polypeptides and polynucleotides encoding the polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or for
 PT genetic analysis of individuals with genetic disorders.
 XX
 PS Claim 2; Fig 9; 218pp; English.
 XX
 CC This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The invention
 CC also comprises a method for producing the proteins of the invention by
 CC recombinant means and antibodies specific for the protein of the
 CC invention. The antibody may be used for detecting the PRO proteins of the
 CC invention and may be used to modify their activity. polynucleotides may
 CC be used as hybridisation probes for a cDNA library to isolate the full-
 CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
 CC probes for mapping the gene which encodes that PRO and for genetic
 CC analysis of individuals with genetic disorders, in assays to identify
 CC other proteins or molecules involved in binding reaction, to generate
 CC transgenic animals or knock-out animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides are
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The sequences may also be used to detect
 CC overexpression on PRO polypeptides in cancerous tumours and for screening

CC for differentially expressed genes using microarray technology. The
 CC present sequence represents a cDNA encoding a human PRO protein of the
 CC invention
 XX
 SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
 Query Match 97.5%; Score 1468; DB 6; Length 2482;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 9 CACGAGCAGAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTGGGCAACAACAAC 68
 DB 995 CCCACGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTGGGCAACAACAAC 1054
 QY 69 TACCTTCGGGAAGAAGAGTGCATTCTAGCCTGTGCGGGTGTGCAAGGTGGCCTTTGAGA 128
 DB 1055 TACCTTCGGGAAGAAGAGTGCATTCTAGCCTGTGCGGGTGTGCAAGGTGGCCTTTGAGA 1114
 QY 129 GGCAGCTCTGGGGCTCAGGGGACTTTCCTCCAGGGGCCCCCTCCATGGAAGGCGCATCCA 188
 DB 1115 GGCAGCTCTGGGGCTCAGGGGACTTTCCTCCAGGGGCCCCCTCCATGGAAGGCGCATCCA 1174
 QY 189 GTGTCTCTGGCACCTGTCAAGCCACCCAGTTCCTGCTGCAAGATGGCTGCTGCATCGAC 248
 DB 1175 GTGTCTCTGGCACCTGTCAAGCCACCCAGTTCCTGCTGCAAGATGGCTGCTGCATCGAC 1234
 QY 249 AGTTTCTGTGAGTGTGACGACACCCCACTGCCCCGACGGCTCCGACGAGGCTGCCTGT 308
 DB 1235 AGTTTCTGTGAGTGTGACGACACCCCACTGCCCCGACGGCTCCGACGAGGCTGCCTGT 1294
 QY 309 GAAATAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATNTCCCGAGCGCAAAAGGG 368
 DB 1295 GAAATAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATNTCCCGAGCGCAAAAGGG 1354
 QY 369 CACTGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGTGGTACTAC 428
 DB 1355 CACTGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGTGGTACTAC 1414
 QY 429 AACCCCTTCAGCGAACACTGCGCCGCTTTACCTATGTTGGTGTGTACGGCAACAAGAAC 488
 DB 1415 AACCCCTTCAGCGAACACTGCGCCGCTTTACCTATGTTGGTGTGTATGGCAACAAGAAC 1474
 QY 489 AACTTTGAGGAAGAGCAGCTGCTCGAGTCTTGTGCGGCGATCTCCAAGAAGGATGTG 548
 DB 1475 AACTTTGAGGAAGAGCAGCTGCTCGAGTCTTGTGCGGCGATCTCCAAGAAGGATGTG 1534
 QY 549 TTTGGCCTGAGGCGGGAATCCCATTTCCAGCACAGGCTCTGTGGAGATGGCTGTGCA 608
 DB 1535 TTTGGCCTGAGGCGGGAATCCCATTTCCAGCACAGGCTCTGTGGAGATGGCTGTGCA 1594
 QY 609 GTGTCTCTGGTCTATCTGCAATGTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 668
 DB 1595 GTGTCTCTGGTCTATCTGCAATGTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 1654
 QY 669 AACGAGAGAAAGGACTTCCACGGACACCAACCAACCAACCAACCAACCAACCAACCAAC 728
 DB 1655 AACGAGAGAAAGGACTTCCACGGACACCAACCAACCAACCAACCAACCAACCAACCAAC 1714
 QY 729 ACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCAACCAACCAACCAACCA 788
 DB 1715 ACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCAACCAACCAACCAACCA 1774
 QY 789 TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTTCTTCCCAAGGAGGAGGCC 848
 DB 1775 TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCTTCTTCCCAAGGAGGAGGCC 1834
 QY 849 TGGGCTGGGAAAAAACTTTGGAACCAAGACTCTTGGCCTGTTTCCAGGCGCCCACTGTGCCTCA 908
 DB 1835 TGGGCTGGGAAAAAACTTTGGAACCAAGACTCTTGGCCTGTTTCCAGGCGCCCACTGTGCCTCA 1894
 QY 909 GAGACGAGGCTCCAGCCCTCTTGGAGAGTCTCAGTAAAGCTCAGCTCCTGAGAAAGC 968
 DB 1895 GAGACGAGGCTCCAGCCCTCTTGGAGAGTCTCAGTAAAGCTCAGCTCCTGAGAAAGC 1954

QY 69 TACCTTCGGGAAGAGAGTGCATTTCTAGCCTGTGCGGGTGTGCAAGGTGGGCTTTTGAGA 128
Db 1055 TACCTTCGGGAAGAGAGTGCATTTCTAGCCTGTGCGGGTGTGCAAGGTGGGCTTTTGAGA 1114
QY 129 GGCAGCTCTGGGCTCAGCGCATTTTCCCGAGGCCCCCTCCATGGAAGGCGCCATCCA 188
Db 1115 GGCAGCTCTGGGCTCAGCGCATTTTCCCGAGGCCCCCTCCATGGAAGGCGCCATCCA 1174
QY 189 GTGTGCTCTGGCACCTGTGAGCCACCCCACTGCGCTGAGCAATGGCTGCTGATCGAC 248
Db 1175 GTGTGCTCTGGCACCTGTGAGCCACCCCACTGCGCTGAGCAATGGCTGCTGATCGAC 1234
QY 249 AGTTTCTCTGAGTGTGACGACACCCCACTGCGCTGAGCAATGGCTGCTGATCGAC 308
Db 1235 AGTTTCTCTGAGTGTGACGACACCCCACTGCGCTGAGCAATGGCTGCTGATCGAC 1294
QY 309 GAAAAATACACGAGTGTGACGAGCTCCAGCGCATCCATTTCCCGAGCGACAAAGGG 368
Db 1295 GAAAAATACACGAGTGTGACGAGCTCCAGCGCATCCATTTCCCGAGCGACAAAGGG 1354
QY 369 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCTGGTACTAC 428
Db 1355 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCTGGTACTAC 1414
QY 429 AACCCCTTCAGCGAACTGCGCCCGCTTACCTATGGTGGTGTGTTACGCGCAACAAGAC 488
Db 1415 AACCCCTTCAGCGAACTGCGCCCGCTTACCTATGGTGGTGTGTTACGCGCAACAAGAC 1474
QY 489 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGCGCATCTCCAGAAAGGATGTG 548
Db 1475 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGCGCATCTCCAGAAAGGATGTG 1534
QY 549 TTTGGCCTGAGCGGGAATCCCATTCACAGACAGGCTCTGTGGAGATGGCTGTGCA 608
Db 1535 TTTGGCCTGAGCGGGAATCCCATTCACAGACAGGCTCTGTGGAGATGGCTGTGCA 1594
QY 609 GTGTTCTCTGTCATCTGCATTTGTGGTGTGAGGAGTCTTGGGTTACTGCTTCTCAAG 668
Db 1595 GTGTTCTCTGTCATCTGCATTTGTGGTGTGAGGAGTCTTGGGTTACTGCTTCTCAAG 1654
QY 669 AACAGAGAAAGGACTTCCAGGACACACACACACACACACACACACACACACACACAC 728
Db 1655 AACAGAGAAAGGACTTCCAGGACACACACACACACACACACACACACACACACACAC 1714
QY 729 ACTGTCTCCACTACCGAGACACGAGACACCTGGCTTATACACACACACACACACACAC 788
Db 1715 ACTGTCTCCACTACCGAGACACGAGACACCTGGCTTATACACACACACACACACACAC 1774
QY 789 TGAGCCTGGGTCTCACCGCTCTCACCTGGCTTCTCTGCTTGCACAGGCGAGAGGC 848
Db 1775 TGAGCCTGGGTCTCACCGCTCTCACCTGGCTTCTCTGCTTGCACAGGCGAGAGGC 1834
QY 849 TGGGCTGGGAAACCTTTGGAACACGAGTCTTGGCTTCTTCCAGGCGGCTGTGCTCA 908
Db 1835 TGGGCTGGGAAACCTTTGGAACACGAGTCTTGGCTTCTTCCAGGCGGCTGTGCTCA 1894
QY 909 GAGACAGGGCTCCAGGCTCTTGGAGAGTCTCAGCTAAGCTCAGCTGAGAGAAAGC 968
Db 1895 GAGACAGGGCTCCAGGCTCTTGGAGAGTCTCAGCTAAGCTCAGCTGAGAGAAAGC 1954
QY 969 TCAAGGTTTGGAGGAGCAGAAACCTTGGGCGCAGAGTACAGACTAGATGGACCTG 1028
Db 1955 TCAAGGTTTGGAGGAGCAGAAACCTTGGGCGCAGAGTACAGACTAGATGGACCTG 2014
QY 1029 CTTGATAGGAGTTTGGAGAGTGGAGTTTGTCTCTGTTCAAGTGGCTGCTGCTC 1088
Db 2015 CTTGATAGGAGTTTGGAGAGTGGAGTTTGTCTCTGTTCAAGTGGCTGCTGCTC 2074
QY 1089 CTACCCCATGGTGTAGAGAGGAGTGGGTTGGTGTGTCAGACCTGGAGGCGCCCAACCT 1148
Db 2075 CTACCCCATGGTGTAGAGAGGAGTGGGTTGGTGTGTCAGACCTGGAGGCGCCCAACCT 2134
QY 1149 GTCTCTCCGAGCTCTCTCTCCATGCTGTGCGCCCGGCTGGGAGGAGGACTTCCCTGT 1208

Db 2135 GTCTCCGAGCTCTCTTCCATGCTGTGCGCCCGGCTGGAGGAGGACTTCCCTGT 2194
QY 1209 GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTATTTATGCTGTGGCATGGGTGAGAG 1268
Db 2195 GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTATTTATGCTGTGGCATGGGTGAGAG 2254
QY 1269 GAGGGAAGAGGCTGTTTGGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328
Db 2255 GAGGGAAGAGGCTGTTTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2314
QY 1329 CTCTGCCCTTGATCAGCCCGCCTGCTGCTAGACAGAGAGGAGGAGCTCA 1388
Db 2315 CTCTGCCCTTGATCAGCCCGCCTGCTGCTAGACAGAGAGGAGGAGGCTCA 2374
QY 1389 GCTGATTCGCGAGCCCGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1448
Db 2375 GCTGATTCGCGAGCCCGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2434
QY 1449 GGGTAATAAAAGTGGTTTGTGGAAAAAATAAAATAAAATAAAATAAAATAAA 1492
Db 2435 GGGTAATAAAAGTGGTTTGTGGAAAAAATAAAATAAAATAAAATAAAATAAAATAAA 2478

RESULT 8

ID ADA01277 standard; cDNA; 2482 BP.

XX ADA01277;

AC ADA01277;

XX 06-NOV-2003 (first entry)

DT 06-NOV-2003 (first entry)

XX Human PRO polynucleotide #5.

DE Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;

XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;

KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;

KW microvascular endothelial cell; endothelial cell tube formation;

KW sports-related joint problem; articular cartilage defect; osteoarthritis;

KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.

XX Homo sapiens.

OS US2003068779-A1.

XX 10-APR-2003.

XX 16-SEP-2002; 2002US-00245107.

XX 09-MAY-2001; 2001US-0290589P.

XX 29-AUG-2001; 2001WO-US027099.

XX 18-JUL-2002; 2002US-00197942.

XX (GETH) GENENTECH INC.

XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,

XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

XX Fong S;

XX WPI; 2003-625484/59.

XX P-PSDB; ADA01278.

XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for

XX stimulating proliferation of human microvascular endothelial cells, and

XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte

XX cells.

XX Claim 2; Fig 9; 307pp; English.

XX The invention relates to isolated human PRO polypeptides (secreted and

XX transmembrane polypeptides) and the polynucleotides encoding them. The

XX invention also relates to an antibody which specifically binds to a PRO

XX polypeptide, a method for stimulating the release of tumour necrosis

factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polynucleotide of the invention.

Db	1715	ACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATATACCAACCAACACCCGGCCCTC	1774
Qy	789	TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCCTGCTTGCCAAAGGCAGAGGCC	848
Db	1775	TGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCCTGCTTGCCAAAGGCAGAGGCC	1834
Qy	849	TGGGCTGGGAAAACTTTTGGAAACCAAGACTCTTGCCCTGTTTCCAGGCCCACTGTGCCCTCA	908
Db	1835	TGGGCTGGGAAAACTTTTGGAAACCAAGACTCTTGCCCTGTTTCCAGGCCCACTGTGCCCTCA	1894
Qy	909	GAGACCAGGGCTCCAGCCCTCTTTGGAGAAGTCTCAGCTAAGCTCAGTCTCTGAGAAAGC	968
Db	1895	GAGACCAGGGCTCCAGCCCTCTTTGGAGAAGTCTCAGCTAAGCTCAGTCTCTGAGAAAGC	1954
Qy	969	TCAAAGTTTGGAAGGAGCAGAAAAACCTTTGGCCAGAAAGTACCAAGACTAGATGGACCTG	1028
Db	1955	TCAAAGTTTGGAAGGAGCAGAAAAACCTTTGGCCAGAAAGTACCAAGACTAGATGGACCTG	2014
Qy	1029	CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTTGTTTTCTCTGTTCAAAGCTGCCTGTCC	1088
Db	2015	CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTTGTTTTCTCTGTTCAAAGCTGCCTGTCC	2074
Qy	1089	CTACCCCATGGTGCTAGGAAGAGGTGGGGTGGTGTCTAGACCCCTGGAGGCCCCCAACCT	1148
Db	2075	CTACCCCATGGTGCTAGGAAGAGGTGGGGTGGTGTCTAGACCCCTGGAGGCCCCCAACCT	2134
Qy	1149	GTCTCTCCGAGCTCCTCTTCCATGCTGTGGGCCCAAGGGCTGGAGGAAGGACTTCCCTGT	1208
Db	2135	GTCTCTCCGAGCTCCTCTTCCATGCTGTGGGCCCAAGGGCTGGAGGAAGGACTTCCCTGT	2194
Qy	1209	GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTGTTTATTTAATGCTGTGGCATGGGTGAAGAG	1268
Db	2195	GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTGTTTATTTAATGCTGTGGCATGGGTGAAGAG	2254
Qy	1269	GAGGGGAAGAGGCCCTGTTTGGCCCTCTCTATCTCTCTTCCCTTCCCTTCCCTTCCCTT	1328
Db	2255	GAGGGGAAGAGGCCCTGTTTGGCCCTCTCTATCTCTCTTCCCTTCCCTTCCCTTCCCTT	2314
Qy	1329	CTCTGCCCTTGATCAGCCCCCACCCCTGGCCTAGACCAGACAGACAGGCCAGGAGAAGCTCA	1388
Db	2315	CTCTGCCCTTGATCAGCCCCCACCCCTGGCCTAGACCAGACAGACAGGCCAGGAGAAGCTCA	2374
Qy	1389	GCTGCATTCCGAGCCCCCACCCCTCCTAGGTTTCTCCAACTACAGCCCCAGCCCCCACT	1448
Db	2375	GCTGCATTCCGAGCCCCCACCCCTCCTAGGTTTCTCCAACTACAGCCCCAGCCCCCACT	2434
Qy	1449	GGGTATATAAAGTGGTTTGTGGAAAAAATAAAAAAAAAAAAAA	1492
Db	2435	GGGTATATAAAGTGGTTTGTGGAAAAAATAAAAAAAAAAAAAA	2478

RESULT 9
ADA43706

ADAA43706
ID ADAA43706 standard: cDNA: 2482 bp.

XX
AC
ADA43706:

DT 20-NOV-2003 (first entry)

XX Human cdna encoding secreted/transmembrane polypeptide PRO256.

ss; Gene; human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.

05 Homo sapiens.

XX
PN US2003064474-A1.

XX
PD 03-APR-2003

Db 1715 ACTGCTCCACTACCGAGGACACGAGCACCTGGTCTATAACACACACCGGCCCTC 1774
QY 789 TGAGCCTGGGTCTACCGGCTCTCACCTGGCCCTGCTTCCCTGCTTGCAGAGGCC 848
Db 1775 TGAGCCTGGGTCTACCGGCTCTCACCTGGCCCTGCTTCCCTGCTTGCAGAGGCC 1834
QY 849 TGGGCTGGGAAAAAATTTGGAACCCAGACTCTTGCCTGTTTCCAGGCCACTGTGCTCA 908
Db 1835 TGGGCTGGGAAAAAATTTGGAACCCAGACTCTTGCCTGTTTCCAGGCCACTGTGCTCA 1894
QY 909 GAGACGAGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGTCTGAGAAAGC 968
Db 1895 GAGACGAGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGTCTGAGAAAGC 1954
QY 969 TCAAGGTTTGGAGGAGCAGAAACCCCTGGGCCAGAGTACCAGACTAGATGGACCTG 1028
Db 1955 TCAAGGTTTGGAGGAGCAGAAACCCCTGGGCCAGAGTACCAGACTAGATGGACCTG 2014
QY 1029 CCTGCAATAGGAGTTTGGAGGAGTTGGAGTTTGGTTTCTCTCTGTTCAAGCTGCTGTC 1088
Db 2015 CCTGCAATAGGAGTTTGGAGGAGTTGGAGTTTGGTTTCTCTCTGTTCAAGCTGCTGTC 2074
QY 1089 CTACCCCATGGTCTAGGAAGAGGAGTGGGTGGTGTCTAGACCTCTGAGGCCCCCAACCT 1148
Db 2075 CTACCCCATGGTCTAGGAAGAGGAGTGGGTGGTGTCTAGACCTCTGAGGCCCCCAACCT 2134
QY 1149 GTCTCTCCGAGCTCTCTCTCCATGCTGTGCGCCCGAGGCTGGGAGGAGGACTTCCCTGT 1208
Db 2135 GTCTCTCCGAGCTCTCTCTCCATGCTGTGCGCCCGAGGCTGGGAGGAGGACTTCCCTGT 2194
QY 1209 GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTGTTTATTTAATGCTGTGGCATGGTGAAG 1268
Db 2195 GTAGTTTGTGCTGTAAAGAGTTGCTTTTGTGTTTATTTAATGCTGTGGCATGGTGAAG 2254
QY 1269 GAGGGGAAGAGCCCTGTTGGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328
Db 2255 GAGGGGAAGAGCCCTGTTGGCT 2314
QY 1329 CTCTGCCCTTGATAGCCGCCACCCCTGGCCCTAGACCAGCAGACAGAGCCAGGAGAGTCA 1388
Db 2315 CTCTGCCCTTGATAGCCGCCACCCCTGGCCCTAGACCAGCAGACAGAGCCAGGAGAGTCA 2374
QY 1389 GCTGCATTCCGAGCCGCCACCCCAAGTTTCTCCAACTATCAGCCAGCCCGCCCACT 1448
Db 2375 GCTGCATTCCGAGCCGCCACCCCAAGTTTCTCCAACTATCAGCCAGCCCGCCCACT 2434
QY 1449 GGGTAATAAAGTGGTTTGTGGAATAAATAAATAAATAAATAAATAA 1492
Db 2435 GGGTAATAAAGTGGTTTGTGGAATAAATAAATAAATAAATAAATAA 2478

RESULT 11

ID ADA01149 standard; cDNA; 2482 BP.

XX AC ADA01149;

XX DF 06-NOV-2003 (first entry)

XX DE Human PRO polynucleotide #5.

XX KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW cancer; lung; colon; breast; prostate; rectum; kidney; liver;
KW microvascular endothelial cell; endothelial cell tube formation.

OS Homo sapiens.

XX US2003068782-A1.

PN 10-APR-2003.

XX

PF 16-SEP-2002; 2002US-00245851.
XX 27-APR-1999; 99US-0131271P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX (GETH) GENENTECH INC.
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX WPI; 2003-625487/59.
DR P-PSDB; ADA01150.
XX Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX Claim 2; Fig 9; 308pp; English.
XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, rectal, kidney and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in
CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such
CC as tumours, for stimulating and inhibiting proliferation of human
CC microvascular endothelial cells and for inducing endothelial cell tube
CC formation. This sequence represents a human PRO polynucleotide of the
CC invention.

XX SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Query Match 97.5%; Score 1468; DB 8; Length 2482;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGAGGCTGCTGGGCAACAAGAACAC 68
Db 995 CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGAGGCTGCTGGGCAACAAGAACAC 1054
QY 69 TACCTTCGGGGAAGAAGAGTGCAATCTAGCCTGTCCGGGTGTGCAAGTGGGCTTTGAGA 128
Db 1055 TACCTTCGGGGAAGAAGAGTGCAATCTAGCCTGTCCGGGTGTGCAAGTGGGCTTTGAGA 1114
QY 129 GGCAGCTCTGGGGCTCAGGGGACTTCCCCCAGGGGCCCTCCATGGAAGGCGCCATCCA 188
Db 1115 GGCAGCTCTGGGGCTCAGGGGACTTCCCCCAGGGGCCCTCCATGGAAGGCGCCATCCA 1174
QY 189 GTGTGCTCTGGCACCTGTGACGCCACCCAGTTCGGCTGCAGCAATGGCTGTCATCGAC 248
Db 1175 GTGTGCTCTGGCACCTGTGACGCCACCCAGTTCGGCTGCAGCAATGGCTGTCATCGAC 1234
QY 249 AGTTTCTCGAGTGTGACGACACCCCAACTGCCCCGACCGCTCCGACGAGGCTGCCTGT 308
Db 1235 AGTTTCTCGAGTGTGACGACACCCCAACTGCCCCGACCGCTCCGACGAGGCTGCCTGT 1294
QY 309 GAAAAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCGCAAGGG 368
Db 1295 GAAAAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCGCAAGGG 1354

PR 02-JUN-2000; 2000WO-US015264.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GETH) GENENTECH INC.
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Pong S;
 XX
 DR WPI; 2003-585304/55.
 DR P-PSDB; ADA43591.
 XX
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
 PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 2; Fig 9; 352pp; English.
 XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence encodes a PRO protein.
 XX
 SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
 Query Match 97.5%; Score 1468; DB 8; Length 2482;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTGGGCAACAAGAAC 68
 Db
 QY 69 TACCTTCGGGAAGAGAGTGCATTTACGCTGTGGGGTGTGCAAGGTGGCCCTTTGAGA 128
 Db 1055 TACCTTCGGGAAGAGAGTGCATTTACGCTGTGGGGTGTGCAAGGTGGCCCTTTGAGA 1114
 QY 129 GGCAGCTTCGGGCTCAGCGGACATTTCCCGCCAGGCCCCCTCCATGGAAAGCGCCATCCA 188
 Db 1115 GGCAGCTTCGGGCTCAGCGGACATTTCCCGCCAGGCCCCCTCCATGGAAAGCGCCATCCA 1174
 QY 189 GTGTGCTTCGGACCTGTGAGCCCAACCGATTCGGCTGCAGCAATGGCTGCTGCATCGAC 248
 Db 1175 GTGTGCTTCGGACCTGTGAGCCCAACCGATTCGGCTGCAGCAATGGCTGCTGCATCGAC 1234

QY 249 AGTTTCCTGGAGTGTGACGACACCCCAACTGCCCGACGCCCTCCGACGAGGCTGCTGT 308
 Db 1235 AGTTTCCTGGAGTGTGACGACACCCCAACTGCCCGACGCCCTCCGACGAGGCTGCTGT 1294
 QY 309 GAAAAATACACGAGTGGCTTTTACGAGCTCCAGCGCATCCATTTCCCGACGACAAAGGG 368
 Db 1295 GAAAAATACACGAGTGGCTTTTACGAGCTCCAGCGCATCCATTTCCCGACGACAAAGGG 1354
 QY 369 CACTGCGTGGACCTGCGCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCTGTACTAC 428
 Db 1355 CACTGCGTGGACCTGCGCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCTGTACTAC 1414
 QY 429 AACCCCTTCAGCGAACAACCTGCGCCCGCTTTACCTATGTTGGTGTTCACGGCAACAAGAAC 488
 Db 1415 AACCCCTTCAGCGAACAACCTGCGCCCGCTTTACCTATGTTGGTGTTCACGGCAACAAGAAC 1474
 QY 489 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCCGGGCATCTCCAAAGAAGATGTG 548
 Db 1475 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCCGGGCATCTCCAAAGAAGATGTG 1534
 QY 549 TTTGGCCTGAGCGCGGAAATCCCATTTCCAGCAGCAGGCTCTGTGGAGATGGCTGTCCGA 608
 Db 1535 TTTGGCCTGAGCGCGGAAATCCCATTTCCAGCAGCAGGCTCTGTGGAGATGGCTGTCCGA 1594
 QY 609 GTGTTCTCTGCTCATCTGCAATTTGTTGGTGGTAGCCATCTTGGTTACTGCTTCTTCAAG 668
 Db 1595 GTGTTCTCTGCTCATCTGCAATTTGTTGGTGGTAGCCATCTTGGTTACTGCTTCTTCAAG 1654
 QY 669 AACCCAGAGAAAGGACTTCCAGGACACCAACCAACCCACCCACCCACCCAGCTCC 728
 Db 1655 AACCCAGAGAAAGGACTTCCAGGACACCAACCAACCCACCCACCCAGCTCC 1714
 QY 729 ACTGTCTCCACTACCGAGACACGGAGCACTTGTGTCTATTAACCAACCAACCGGCCCTC 788
 Db 1715 ACTGTCTCCACTACCGAGACACGGAGCACTTGTGTCTATTAACCAACCAACCGGCCCTC 1774
 QY 789 TGAGCCTGGGTCTCACCGCTCTCACCTGGCCCTCTGCTTCCAGGAGGAGGCC 848
 Db 1775 TGAGCCTGGGTCTCACCGCTCTCACCTGGCCCTCTGCTTCCAGGAGGAGGCC 1834
 QY 849 TGGGCTGGGAAAAAATTTGGAAACAGACTCTTGGTGTTCAGGCCCTCTGTGCTCA 908
 Db 1835 TGGGCTGGGAAAAAATTTGGAAACAGACTCTTGGTGTTCAGGCCCTCTGTGCTCA 1894
 QY 909 GAGACGAGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGCTCTGAGAAAGC 968
 Db 1895 GAGACGAGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCAGCTCTGAGAAAGC 1954
 QY 969 TCAAAGGTTTGGAGGAGCAGAAACCCCTTGGGCGAGAAAGTACAGACTAGATGACCTG 1028
 Db 1955 TCAAAGGTTTGGAGGAGCAGAAACCCCTTGGGCGAGAAAGTACAGACTAGATGACCTG 2014
 QY 1029 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTTCAAAGCTGCTGTCC 1088
 Db 2015 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTTCAAAGCTGCTGTCC 2074
 QY 1089 CTACCCCATGCTGTAGGAAGAGGAGTGGGGTGTGTGAGCCCTGAGAGGCCCAACCCCT 1148
 Db 2075 CTACCCCATGCTGTAGGAAGAGGAGTGGGGTGTGTGAGCCCTGAGAGGCCCAACCCCT 2134
 QY 1149 GTCCCTCCGAGCTCCTCTTCCATGCTGTGCGCCCGAGGCTGGGAGGAGGACTTCCCTGT 1208
 Db 2135 GTCCCTCCGAGCTCCTCTTCCATGCTGTGCGCCCGAGGCTGGGAGGAGGACTTCCCTGT 2194
 QY 1209 GTAGTTTGTCTGTAAAGAGTTGCTTTTGTATTATTAATGCTGTGGCATGGTGAAGAG 1268
 Db 2195 GTAGTTTGTCTGTAAAGAGTTGCTTTTGTATTATTAATGCTGTGGCATGGTGAAGAG 2254
 QY 1269 GAGGGGAAGAGGCTGTTGGCCTCTCTATCTCTCTTCTCTTCCCGCAAGATTGAGCT 1328
 Db 2255 GAGGGGAAGAGGCTGTTGGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2314

QY 1329 CTCTGCCCCCTTGATCAGCCGCCACCCCTGGCCCTAGACCAGACAGAGCCAGGAGAGCTCA 1388
 Db |||||
 QY 2315 CTCTGCCCCCTTGATCAGCCGCCACCCCTGGCCCTAGACCAGACAGAGCCAGGAGAGCTCA 2374
 Db |||||
 QY 1389 GCTGCATTCGCGAGCCGCCACCCCAAGGTTCTCCAAATCATCAGCCAGCCCGCCCACT 1448
 Db |||||
 QY 2375 GCTGCATTCGCGAGCCGCCACCCCAAGGTTCTCCAAATCATCAGCCAGCCCGCCCACT 2434
 Db |||||
 QY 1449 GGGTAATAAAGTGGTTTGTGGAATAAATAAATAAATAAATAAATAA 1492
 Db |||||
 QY 2435 GGGTAATAAAGTGGTTTGTGGAATAAATAAATAAATAAATAAATAA 2478
 Db |||||

RESULT 14

ADA06852

ID ADA06852 standard; cDNA; 2482 BP.

XX

AC ADA06852;

XX 06-NOV-2003 (first entry)

DT

XX Human PRO polynucleotide #5.

DE

XX Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW bone disorder; cartilage disorder; sports injury; proteoglycan;
 KW cartilage; sports-related joint problem; articular cartilage defect;
 KW osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder;
 KW thalassaemia; immune system cell infiltration; cancer; vulnary;
 KW antianaemic; osteopathic; antirheumatic; antiarthritic.

XX Homo sapiens.

OS

XX US2003068781-A1.

PN

XX 10-APR-2003.

PD

XX 16-SEP-2002; 2002US-00245771.

PF

XX 03-AUG-1999; 99US-0146843P.

PR 15-MAY-2000; 2000WO-US013358.

PR 29-AUG-2001; 2001WO-US027099.

PR 18-JUL-2002; 2002US-00197942.

XX (GETH) GENENTECH INC.

PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

PI Fong S;

PI WPI; 2003-625486/59.

XX P-PSDB; ADA06853.

DR

XX Novel secreted and transmembrane polypeptides, PRO polypeptides useful

PT for stimulating proliferation or differentiation of chondrocyte cells and

PT inducing endothelial cell tube formation.

XX Claim 2; Fig 9; 307pp; English.

PS

XX The invention relates to isolated human PRO polypeptides (secreted and

CC transmembrane polypeptides) and the polynucleotides encoding them. The

CC invention also relates to an antibody which specifically binds to a PRO

CC polypeptide, a method for stimulating the release of tumour necrosis

CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the

CC proliferation or differentiation of chondrocyte cells and a method for

CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,

CC colon, breast, prostate, rectal, cervical and liver tumours). The

CC polynucleotides are useful in molecular biology, including uses as

CC hybridisation probes, in chromosome and gene mapping, in generating

CC antisense RNA and DNA and in gene therapy. The polynucleotides may also

CC be used in preparing PRO polypeptides by recombinant techniques and in

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CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for inducing endothelial cell
 CC tube formation and for treating various bone and/or cartilage disorders
 CC such as sports injuries and arthritis. PRO polypeptides which stimulate
 CC the release of proteoglycans from cartilage are useful for treating
 CC sports-related joint problems, articular cartilage defects,
 CC osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful
 CC for treating various mammalian haemoglobin-associated disorders such as
 CC various thalassaemias and conditions which may benefit from enhanced
 CC local immune system cell infiltration. This sequence represents a human
 CC PRO polynucleotide of the invention.

XX
 SQ Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Query Match 97.5%; Score 1468; DB 8; Length 2482;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Job time : 645 secs

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OM nucleic - nucleic search, using sw model

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Perfect score: 1505
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
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- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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7	1468	97.5	2482	6	AX574482	AX574482 Sequence
8	1468	97.5	2482	9	AY358969	AY358969 Homo sapi
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14	1344.6	89.3	2399	9	AB000095	AB000095 Homo sapi
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17	886.4	58.9	115793	9	AC025166	AC025166 Homo sapi
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ALIGNMENTS

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ACCESSION	BD063229	Secreted human proteins.				
VERSION	BD063229.1	GI:22608832				
KEYWORDS	JP 2001505783-A/4.					
SOURCE	unidentified					
ORGANISM	unidentified					
REFERENCE	1 (bases 1 to 1505)					
AUTHORS	Escobedo, J., Hu, Q., Garcia, P., Williams, L.T. and Kothakota, S.					
TITLE	Secreted human proteins					
JOURNAL	Patent: JP 2001505783-A 4 08-MAY-2001;					
	CHIRON CORP					

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AX454456

LOCUS 2482 bp DNA linear PAT 06-JUL-2002

DEFINITION Sequence 41 from Patent WO0208284.

ACCESSION AX454456

VERSION AX454456.1 GI:21713852

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

JOURNAL Patent: WO 0208284-A 41 31-JAN-2002; Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US); Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US); Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William I. (US)

FEATURES

source Location/Qualifiers

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ORIGIN

Query Match 97.5%; Score 1468; DB 6; Length 2482;

Best Local Similarity 99.3%; Pred. No. 0;

Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Db 1055 TACCTTCGGGAAGAGAGTGCATTTAGCCTGTGCGGGTGTGCAAGGTGGCTTTGAGA 1114

Qy 129 GGCAGCTCTGGGCTCAGCGGACTTTCCCGCAGGCTTCCATGGAAGGCGCATCCA 188

Db 1115 GGCAGCTCTGGGCTCAGCGGACTTTCCCGCAGGCTTCCATGGAAGGCGCATCCA 1174

Qy 189 GTGTGCTCTGGCAGCTGTGAGCCACCCAGTTCGCTGCGAGCAATGGCTGTGCGATCGAC 248

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LOCUS AX490934 2482 bp DNA linear PAT 16-AUG-2002

DEFINITION Sequence 41 from Patent WO0200690.

ACCESSION AX490934

VERSION AX490934.1 GI:22323804

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

JOURNAL Patent: WO 0200690-A 41 03-JAN-2002; Genentech, Inc. (US)

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Location/Qualifiers

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LOCUS AR123705 1870 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 6 from patent US 6171790.
ACCESSION AR123705

VERSION AR123705.1 GI:14109066
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1870)
AUTHORS Hillman,J.L., Tang,Y.Tom., Lal,P., Corley,N.C., Guegler,K.J. and
Patterson,C.
TITLE Human protease associated proteins
JOURNAL Patent: US 6171790-A 6 09-JAN-2001;
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DEFINITION Human protease associated proteins.
ACCESSION BD205506
VERSION BD205506.1 GI:33015276
KEYWORDS JP 2002513572-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1870)
AUTHORS Hillman,J.L., Tang,T.Y., Lal,P., Corley,N.C., Guegler,K.J. and
Patterson,C.
TITLE Human protease associated proteins
JOURNAL Patent: JP 2002513572-A 2 14-MAY-2002;
COMMENT INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002513572-A/2
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PR 01-MAY-1998 US 09/071709
PI JENNIFER L HILLMAN,TOM Y TANG,PREETI LAL,NEIL C CORLEY,KARL J
PI GUEGLER,
PI CHANDRA PATTERSON

PC C12N15/09,A61K38/00,A61K45/00,A61P19/02,A61P35/00,A61P37/02,
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LOCUS	Homo sapiens serine protease inhibitor, Kunitz type 1, transcript variant 2, mRNA (cdna clone MGC:15571 IMAGE:3140292), complete cds.				
DEFINITION	BC018702				
ACCESSION	BC018702.1				
VERSION	GI:17511685				
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2486)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				

JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 2486)
Strausberg R.
Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
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ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Shimomura,T., Denda,K., Kitamura,A., Kawaguchi,T., Kito,M., Kondo,J., Kagaya,S., Qin,L., Takata,H., Miyazawa,K. and Kitamura,N.
TITLE Hepatocyte growth factor activator inhibitor, a novel Kunitz-type serine protease inhibitor
JOURNAL J. Biol. Chem. 272 (10), 6370-6376 (1997)
MEDLINE 97197808
PUBMED 9045658
REFERENCE 2 (bases 1 to 2399)
AUTHORS Denda,K.
TITLE Direct Submission
JOURNAL Submitted (24-DEC-1996) Kimitoshi Denda, Tokyo Institute of Technology, Department of Life Science; 4259 Nagatsuta, Midori-ku, Yokohama, Kanagawa 227, Japan (E-mail:kdenda@bio.titech.ac.jp, Tel:45-924-5702, Fax:45-924-5771)
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REFERENCE 1
AUTHORS Yuqiu,J. and Mitcham,J.L.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0078960-A 24 28-DEC-2000;
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Search completed: April 22, 2004, 07:00:18
Job time : 6031 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 22, 2004, 08:10:04 ; Search time 2501 Seconds
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Title: US-09-935-390A-23
Perfect score: 1167
Sequence: 1 MERRHPVSGTCQPTQFRCS.....TVSTTTEDEHLVYNHTTRPL 206

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09935390/runat_20042004_144850_10396/app_query.fasta_1.391
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09935390 @CGN_1_1_3437 @runat_20042004_144850_10396 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

- Database :
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_mam:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*
 - 28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1167	100.0	888	13	BQ687222	BQ687222 AGENCOURT
2	1167	100.0	1183	9	AL558524	AL558524 AL558524
3	1164	99.7	1004	13	BX360990	BX360990 BX360990
4	1156	99.1	1201	13	BX385810	BX385810 BX385810
5	1154	98.9	635	12	BM820520	BM820520 K-EST0089
6	1141	97.8	862	14	CA488310	CA488310 AGENCOURT
7	1074.5	92.1	973	14	CA488377	CA488377 AGENCOURT
8	1063.5	91.1	925	12	BG291726	BG291726 60388738
9	1031	88.3	663	12	BG697670	BG697670 602660928
10	1016	87.1	1201	13	BX336602	BX336602 BX336602
11	1008.5	86.4	882	10	BE794925	BE794925 601589675
12	999	85.6	2155	11	AK017342	AK017342 Mus muscu
13	991	84.9	948	13	BX369479	BX369479 BX369479
14	945	81.0	647	14	CF146773	CF146773 UI-HF-CB0
15	892.5	76.5	1201	13	BX334952	BX334952 BX334952
16	888	76.1	923	13	BQ690456	BQ690456 AGENCOURT
17	885.5	75.9	890	12	BG746579	BG746579 602703881
18	870	74.6	1201	9	AL550947	AL550947 AL550947
19	867	74.3	811	12	BG679448	BG679448 602627456
20	863.5	74.0	695	12	BI871239	BI871239 603395142
21	849	72.8	899	14	CA489864	CA489864 AGENCOURT
22	846	72.5	740	10	BE740145	BE740145 601595087
23	846	72.5	1836	11	BC020485	BC020485 Mus muscu
24	842	72.2	563	14	CF139502	CF139502 UI-HF-CB0
25	842	72.2	939	13	BQ930531	BQ930531 AGENCOURT
26	835	71.6	1092	12	BM550087	BM550087 AGENCOURT
27	832.5	71.3	816	12	BI910513	BI910513 603067895
28	807	69.2	1010	14	CB236863	CB236863 AGENCOURT
29	805	69.0	849	12	BG386824	BG386824 602455103
30	799.5	68.5	1060	13	BQ892320	BQ892320 AGENCOURT
31	798	68.4	1030	29	AY416947	AY416947 Pan trogl
32	798	68.4	1336	29	AY416946	AY416946 Homo sapi
33	796	68.2	611	12	EM008657	EM008657 603618324
34	784	67.2	411	12	BM844926	BM844926 K-EST0123
35	784	67.2	775	12	BG387116	BG387116 602455829
36	780	66.8	592	12	BI346114	BI346114 375143 MA
37	768.5	65.9	458	10	BE616990	BE616990 601441583
38	738.5	63.3	923	10	BE742267	BE742267 601575685
39	737	63.2	987	9	AL540329	AL540329 AL540329
40	736	63.1	731	12	BG821636	BG821636 602727640
41	727.5	62.3	643	13	BU696712	BU696712 LL2in1273
42	720	61.7	555	12	BG609825	BG609825 323809 MA
43	714	61.2	621	13	BQ190036	BQ190036 UI-R-CN1-
44	708.5	60.7	1201	13	BX336937	BX336937 BX336937
45	693.5	59.4	764	10	BE281028	BE281028 601159195

ALIGNMENTS

RESULT 1
BQ687222
LOCUS
DEFINITION BQ687222 888 bp mRNA linear EST 15-JUL-2002
5', mRNA sequence. AGENCOURT_8047251 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207448
ACCESSION BQ687222
VERSION BQ687222.1 GI:21812538
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 888)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM2363 row: 1 column: 17
High quality sequence stop: 675.
Location/Qualifiers
1..888
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6207448"
/tissue type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 1.61e-109 Length: 888
Score: 1167.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-935-390A-23 (1-206) x BQ687222 (1-888)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 93 ATGGAAGCGCCATCCAGTGTCTGGCAGCTGTGCACCTGTGCAGCCACCCAGTCCGCTGCAGC 152
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
DB 153 AATGGTGTCTGATCGACAGTTCTCTGGAGTGTGACGACACCCCACTGCCCGACGCC 212
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 213 TCCGACGAGGCTGCCTGTGAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 272
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 273 TTCCCAAGTGACAAAGGGCACTGGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 332
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
DB 333 ATCCCGCGCTGGTACTACAACCCCTTCAGCGAACACTGCGCCGCTTTACCTATGGTGGT 392
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGluGlnGlnCysLeuGluSerCysArgGly 120
DB 393 TGTATGGCAACACAGAAACACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGC 452
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
DB 453 ATCTCCAGAAAGGATGTGTTTGGCTGAGCGCGGAAATCCCAATCCAGACAGGCTCT 512
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160

Db 513 GTGGAGATGGCTGTGCAGTGTCTCTGTCATCTGCATTGTGGTGGTAGCCATCTTG 572
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 573 GGTTACTGCTTCTTCAAGAACCAGAGAAGGACTTCCACGGACACCAACCCACCA 632
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 633 CCCACCCCTGCCAGTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 692
QY 201 HistThrThrArgProLeu 206
Db 693 CACACCACCCGCCCTC 710

RESULT 2

AL558524

LOCUS

DEFINITION

AL558524 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED

AL558524 Homo sapiens cDNA clone CS0DJ006YG14 5-PRIME, mRNA sequence.

AL558524

AL558524.2 GI:31280322

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1183)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12903126.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7854.f For

more information about this cluster, see

[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DJ006BD07QP1&cluster=7854.f)

cgi-bin/cluster.cgi?seq=CS0DJ006BD07QP1&cluster=7854.f. Contact :

Peng Liang Email: fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/InvitrogenCorporation1600>

Paraday Avenue Genoscope sequence ID : CS0DJ006BD07QP1.

Location/Qualifiers

1..1183

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DJ006YG14"

/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"

/cell_line="JURKAT"

/clone lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT

10-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 2.41e-109 Length: 1183

Score: 1167.00 Matches: 206

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-935-390A-23 (1-206) x AL558524 (1-1183)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20

Db 281 ATGGAAGCGCCATCCAGTGTCTTGGACCTGTGCAGCCACCCAGTCCGCTGCAGC 340

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Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 341 AATGGCTGCTGCATCGACAGTTCTCTGGAGTGTGACGACACCCCAACTGCCCGCAGGCC 400
Qy 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 401 TCCGACGAGGCTGCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 460
Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 461 TTCCCCAGTGACAAAGGCACTCGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 520
Qy 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 521 ATCCCGCGCTGGTACTACAAACCCCTTCAGCGAACAACCTGCGCGCGCTTTACCTATGGTGT 580
Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db 581 TGTATGGCAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGGC 640
Qy 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db 641 ATCTCAAGAAGGATGTGTTGGCTGAGGCGGGAATCCCATTTCCAGCACAGGCTCT 700
Qy 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db 701 GTGGAGATGGCTGTGCGCAGTGTCTCTGTCATCTGCAATTGGTGTGGTAGCCATCTTG 760
Qy 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 761 GGTACTGCTTCTTCAAGAACCAAGAGAAAGGACTTCCACGACACACCACCCACCA 820
Qy 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 821 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGAGCACCTGGTCTATAAC 880
Qy 201 HistThrArgProLeu 206
Db 881 CACACCACCGGCGCCCTC 898
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```
RESULT 3
BX360990 1004 bp mRNA linear EST 05-MAY-2003
DEFINITION
BX360990 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI078Y010 5-PRIME, mRNA sequence.
BX360990
ACCESSION
BX360990.1 GI:30380508
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
```

```
REFERENCE
AUTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
```

```
cgibin/cluster.cgi?seq=CS0DI078BH05QP1&cluster=7854.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DI078BH05QP1.
```

```
FEATURES
source
1..1004
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone="CS0DI078Y010"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
```

ORIGIN

```
Alignment Scores:
Pred. No.: 3.9e-109 Length: 1004
Score: 1164.00 Matches: 205
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.51% Mismatches: 0
Query Match: 99.74% Indels: 0
DB: 13 Gaps: 0

US-09-935-390A-23 (1-206) x BX360990 (1-1004)
Qy 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 214 ATGGAAGGCGCCATCCAGTGTGCTCTGGACCTGTCAGCCACCCAGTTCGGCTGCAGC 273
Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 274 AATGGCTGCTGCATCGACAGTTTCTGGAGTGTGACGACACCCCACTGCCCGCAGGCC 333
Qy 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 334 TCCGACGAGGCTGCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 393
Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 394 TTCCCCAGCGACAAAGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 453
Qy 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 454 ATCCCGCGCTGGTACTACAAACCCCTTTCAGCGAACAACCTGCGCCGCTTTACCTATGGTGT 513
Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db 514 TGTATGGCAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGGC 573
Qy 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db 574 ATCTCAAGAAGGATGTGTTGGCTTGAGCGCGGAAATCCCATTTCCCAACACAGGCTCT 633
Qy 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db 634 GTGGAGATGGCTGTGCGCAGTGTCTCTGTCATCTGTCATTTGGTGTGGTAGCCATCTTG 693
Qy 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 694 GGTACTGCTTCTTCAAGAACCAAGAGAAAGGACTTCCACGACACACCACCCACCA 753
Qy 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 754 CCCACCCCTGCCAGTCCACTGTCTCCACTACCGAGGACACGAGCACCTGGTCTATAAC 813
Qy 201 HistThrArgProLeu 206
Db 814 CACACCACCGGCGCCCTC 831
```

RESULT 4

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BX385810
LOCUS
DEFINITION
BX385810 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI005YB10 5-PRIME, mRNA sequence.
BX385810
ACCESSION
BX385810.1 GI:30455372
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
```

```
BX385810 1201 bp mRNA linear EST 08-MAY-2003
DEFINITION
BX385810 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI005YB10 5-PRIME, mRNA sequence.
```

```
ACCESSION
BX385810
VERSION
BX385810.1 GI:30455372
KEYWORDS
EST.
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1A1002ZB06Q1&cluster=7854.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS1A1002ZB06Q1.

FEATURES

source

1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI005YB10"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 3.34e-108 Length: 1201
Score: 1156.00 Matches: 204
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.06% Indels: 0
DB: 13 Gaps: 0

US-09-935-390A-23 (1-206) x BX385810 (1-1201)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 365 ATGGAAGGCGCCATCCAGTGTGCTCTGGCACCTGTGAGCCACCCAGTTCGCGTGCAGC 424
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
DB 425 AATGGCTGCTGCATCGACAGTTTCCTGGAGTGTGACGACACACCCCACTGCCGAGCC 484
QY 41 SerAspGluAlaAlaCysGluYsTyThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 485 TCCGACGAGGCTGCCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 544
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 545 TTCCCGACGACAAAGGGCACTGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 604
QY 81 IleProArgTrpTyTyAsnProPheSerGluHisCysAlaArgPheThrTyGlyGly 100
DB 605 ATCCCGGCTGGTACTACACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGCTGGT 664
QY 101 CysTyGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
DB 665 TGTTCGGCAACAAGAACACTTTGAGGAGAGCAGCAGTGCCTCGAGTCTTGTTCGCGGC 724
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
DB 725 ATCTCCAGAAGGATGTGTTGGCTGAGCGGGAAATCCCATTTCCAGCACAGGCTCT 784
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
DB 785 GTGGAGATGGCTGTGCGAGTGTCTGGTCATCTGCATTTGTGGTGTGGTAGCCATCTTG 844

QY 161 GlyTyrCysPheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
DB 845 GGTACTGCTTCTTCAAGAACCCAGAAAGGACTTCCACGGACACCAACCCACCA 904
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyAsn 200
DB 905 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGAGCAGCCTGGTCTATAAM 964
QY 201 HisThrThrArgPro 205
DB 965 CACACGACGCGGCC 979

RESULT 5

BM820520

LOCUS

DEFINITION

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 7 row: H column: 10

High quality sequence stop: 635.

Location/Qualifiers

1..635

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S20T665307-7-H10"

/sex="M"

/lab_host="Top10F"

/clone_lib="S20T665307"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;

Site 2: NotI; The poly (A) + RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then decapped

with tabacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F' by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

ORIGIN

Alignment Scores:

Pred. No.: 2.2e-108 Length: 635
Score: 1154.00 Matches: 205
Percent Similarity: 99.52% Conservative: 0
Best Local Similarity: 99.52% Mismatches: 0
Query Match: 98.89% Indels: 1

DB:	12	Gaps:	0
US-09-935-390A-23 (1-206) x BM820520 (1-635)			
QY	1	MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer	20
DB	15	ATGGAAAGGCGCCATCCAGTGTGCTCTGACACCTGTGACCCACCCAGTTCGGTGCAGC	74
QY	21	AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla	40
DB	75	AATGGCTGCTGCATCGACAGTTTCTCTGGAGTGTGACGACACCCCACTGCCCGACGCC	134
QY	41	SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis	60
DB	135	TCCGACGAGGCTGCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGGCTCCAT	194
QY	61	PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer	80
DB	195	TTCCCCAGTGAACAAGGGCACTGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGC	254
QY	81	IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly	100
DB	255	ATCCCGCGCTGCTACTACAAACCCCTTCAGCGAACAATCCCACTTCCAGCACAGGCTCT	314
QY	101	CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly	120
DB	315	TGTTATGGCAACAAGAACAACTTTGAGGAGAGCAGCAGTGCCTCGAGTCTTGTGCGGC	374
QY	121	IleSerLysLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer	140
DB	375	ATCTCCAAGAGGATGTTTGGCTTGAGCGGGAATCCCACTTCCAGCACAGGCTCT	434
QY	141	ValGluMetAlaValAlaValPheLeuValIleCysIle-ValVal-AlaIleLe	160
DB	435	GTGGAGATGGCTGTCGAGTGTCTCTGTCATCTGTCATTTGGTGGTGGTGGTGGTGGT	494
QY	160	uGlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProp	180
DB	495	GGTTACTGCTTCTCAAGAACCAAGAGAAAGGACTTCCACGGACACCAACCAACCCACC	554
QY	180	oProThrProAlaSerSerThrValSerThrGluAspThrGluHisLeuValTyrAs	200
DB	555	ACCCACCCCTGCCAGTCCACTGTCTCCACTACCGAGGACACGGAGCACTGGTCTATAA	614
QY	200	nHisThrThrArgProLeu	206
DB	615	CCACACCAACCCGGCCCTC	633
RESULT 6	CA488310	862 bp	linear
LOCUS	AGENCOURT_10807835	MAPcL	Homo sapiens
DEFINITION	AGENCOURT_10807835	MAPcL	Homo sapiens
ACCESSION	CA488310	GI:24949829	
VERSION	CA488310.1	GI:24949829	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 862)		
JOURNAL	NIH-MGC http://mgi.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs@mail.nih.gov		
	Tissue procurement: Kristi A. Egland, Ira Pastan		
	CDNA Library Preparation: Invitrogen Corp		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
Plate: LLAM14278 row: p column: 10			
High quality sequence stop: 600.			
Location/Qualifiers			
1. .862			
/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="taxon:9606"			
/clone="IMAGE:6720058"			
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,			
hTERT-HME1, LNCaP"			
/lab_host="EMDH10B"			
/clone_lib="MAPcL"			
/note="Vector: pCMV-SPORT6; Site 1: EcorV; Site 2: Not I;			
Subtracted with brain, liver, lung, kidney and muscle.			
Directionally cloned. Priming method: oligo-dT. Average			
Insert size: 1800 bp. Library amplification: 26,000 fold.			
Kristi A. Egland, James J. Vincent, Robert Strausberg,			
Bungkook Lee & Ira Pastan: Discovery of new breast			
cancer genes encoding membrane and secreted proteins.			
Manuscript submitted."			
ORIGIN			
Alignment Scores:	7.35e-107	Length:	862
Pred. No.:	1141.00	Matches:	206
Score:	99.04%	Conservative:	0
Percent Similarity:	99.04%	Mismatches:	0
Best Local Similarity:	97.77%	Indels:	2
Query Match:	14	Gaps:	0
DB:	US-09-935-390A-23 (1-206) x CA488310 (1-862)		
QY	1	MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer	20
DB	135	ATGGAAAGGCGCCATCCAGTGTGCTCTGACACCTGTGACCCACCCAGTTCGGTGCAGC	194
QY	21	AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla	40
DB	195	AATGGCTGCTGCATCGACAGTTTCTCTGGAGTGTGACGACACCCCACTGCCCGACGCC	254
QY	41	SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis	60
DB	255	TCCGACGAGGCTGCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGGCTCCAT	314
QY	61	PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer	80
DB	315	TTCCCCAGTGAACAAGGGCACTGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGC	374
QY	81	IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly	100
DB	375	ATCCCGCGCTGCTACTACAAACCCCTTCAGCGAACAATCCCACTTCCAGCACAGGCTCT	434
QY	101	CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly	120
DB	435	TGTTATGGCAACAAGAACAACTTTGAGGAGAGCAGCAGTGCCTCGAGTCTTGTGCGGC	494
QY	121	IleSerLysLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer	140
DB	495	ATCTCCAAGAGGATGTTTGGCTTGAGCGGGAATCCCACTTCCAGCACAGGCTCT	554
QY	141	ValGluMetAlaValAlaValPheLeuValIleCysIle-ValVal-AlaIleLe	160
DB	555	GTGGAGATGGCTGTCGAGTGTCTCTGTCATCTGTCATTTGGTGGTGGTGGTGGTGGT	614
QY	160	euGlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProp	180
DB	615	TGGTACTGCTTCTCAAGAACCAAGAGAAAGGACTTCCACGGACACCAACCAACCCACC	674
QY	180	roProThrProAlaSerSerThrValSerThrGluAspThrGluHisLeuValTyrA	200
DB	675	CACCCACCCCTGCCAGTCCACTGTCTCCACTACCGAGGACACGGAGCACTGGTCTATA	734
QY	200	snHisThrThrArgProLeu	206

||||| 364 GGGCACTGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGTGGTAC 423

QY 86 TyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGlyCysTyrGlyAsnLys 105

Db 424 TACAACCCCTTACGCGAACACTGCGCCCGCTTACCTATGGTGGTTGTATGGCAACAAG 483

QY 106 AsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGlyIleSerLysLysAsp 125

Db 484 AACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGCATCTCCAAAGAAGGAT 543

QY 126 ValPheGlyLeuArgArgGluIleProIleProSerThrGlySerValGluMetAlaVal 145

Db 544 GTGTTTGGCTTGGCGGGAATCCCAATCCAGCACAGGCTCTGTGGAGATGGTGTGTC 603

QY 146 AlaValPheLeuValIleCysIleVal-ValValAlaIleLeuGlyTyrCysPhePh 165

Db 604 GCAGTGTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 663

QY 165 eLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProProProThrProAlaSe 185

Db 664 CAAGAACCAGAGAAAGGACTTCCCGGACACACACACACACACACACACACACACAC 723

QY 185 rSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsnHisThrThrArg-- 204

Db 724 CTCCTCTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATACACACACACCGCGGC 783

QY 205 -ProLeu 206

Db 784 CCTCTG 790

RESULT 8

LOCUS BG291726 925 bp mRNA linear EST 21-FEB-2001

DEFINITION 602388738F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4517528 5', mRNA sequence.

ACCESSION BG291726

VERSION BG291726.1 GI:13049896

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 925)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov> Plate: LLAM10410 row: 1 column: 09 High quality sequence stop: 655. Location/Qualifiers

FEATURES

Source 1..925

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:4517528"

tissue_type="transitional cell papilloma, cell line"

lab_host="DH10B (phage-resistant)"

clone_lib="NIH MGC 93"

note="Organ: bladder; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

||||| 735 ACCACACACCGGCGCCCTC 754

Db CA488377 973 bp mRNA linear EST 14-NOV-2002

AGENCOURT_10809135 MAPcL Homo sapiens cDNA clone IMAGE:6720133 5', mRNA sequence.

ACCESSION CA488377

VERSION CA488377.1 GI:24950090

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 973)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Kristi A. Egland, Ira Pastan CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov> Plate: LLAM14279 row: c column: 13 High quality sequence stop: 598. Location/Qualifiers

FEATURES

Source 1..973

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:6720133"

cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-RME1, LNCaP"

lab_host="EMDH10B"

clone_lib="MAPcL"

note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkok Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."

ORIGIN

Alignment Scores:

Pred. No.: 6.12e-100 Length: 973

Score: 1074.50 Matches: 195

Percent Similarity: 96.06% Conservatives: 0

Best Local Similarity: 96.06% Mismatches: 6

Query Match: 92.07% Indels: 2

DB: 14 Gaps: 1

US-09-935-390A-23 (1-206) x CA488377 (1-973)

QY 6 ProValCysSerGlyThrCysGlnProThrGlnPheArgCysSerAsnGlyCysCysIle 25

Db 184 CCAGTGTGCTCTGGCACCCTGTGAGCCACCCAGTTCGGTGCAGCAATGGCTGTCATC 243

QY 26 AspSerPheLeuGluCysAspAspThrProAsnCysProAspAlaSerAspGluAlaAla 45

Db 244 GACAGTTCTTGGAGTGTGACGACACCCCACTGCCCGAGCCTCCGACGAGCTGCC 303

QY 46 CysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHisPheProSerAspLys 65

Db 304 TGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGAGTGACAA 363

QY 66 GlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSerIleProArgTrpTyr 85

Alignment Scores:

Pred. No.: 7.74e-99 Length: 925
Score: 1063.50 Matches: 198
Percent Similarity: 96.12% Conservative: 0
Best Local Similarity: 96.12% Mismatches: 7
Query Match: 91.13% Indels: 3
DB: 12 Gaps: 1

US-09-935-390A-23 (1-206) x BG291726 (1-925)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 33 ATGGAAGCGCCCATCCAGTGTCTCTGGACCTGTGAGCCACCCAGTTCGGTGCAGC 92
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
DB 93 AATGGCTGCTGCATCGACAGTTCTCTGGAGTGTGACGACACCCCAACTGCCCGAGGCC 152
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 153 TCCGACGAGGCTGCTGTGAAAATAACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 212
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 213 TTCCCCAGTGACAAAGGCGACTGCGTGGACTGCCAGACACAGGACTCTGCAAGGAGGC 272
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
DB 273 ATCCCGCGCTGGTACTACACCCCTTCAGGACACTGCGCCGCTTTACCTATGGTGGT 332
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
DB 333 TGTATGGCAACAGAACAACTTTGAGGAGAGCAGCAGTGGCTCGAGTCTTGTGCGGCGC 392
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
DB 393 ATCTCCAGAGAGGATGTGTTGGCTGTGCGGGAATCCCCATTCAGGACACAGGCTCT 452
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
DB 453 GTGGAGATGGCTGTGCGAGTGTCTCTGGTCACTGCTGATTTGGTGGTGGTAGCCATCTG 512
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
DB 513 GGTACTGCTTCTCAAGAACCCAGAGAAAGGACTTCCACGGA---CACGAGCACACGAGC 569
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
DB 570 ACCAC-CCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGAGCAGCTG-GTCTATAAC 627
QY 201 HistThrThrArgProLeu 206
DB 628 CACACACCGCGCCCTCTG 645

RESULT 9

BG697670

LOCUS

602660928P1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4803894 5',
mRNA sequence.

ACCESSION

BG697670

VERSION

BG697670.1 GI:13964146

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 663)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10700 row: h column: 07

High quality sequence stop: 662.

FEATURES

source

1..663
/organism="Homo sapiens"
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/clone_lib="NCI CGAP Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1; NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI CGAP Library."

ORIGIN

Alignment Scores:
Pred. No.: 1.08e-95 Length: 663
Score: 1031.00 Matches: 185
Percent Similarity: 97.37% Conservative: 0
Best Local Similarity: 97.37% Mismatches: 4
Query Match: 88.35% Indels: 1
DB: 12 Gaps: 0

US-09-935-390A-23 (1-206) x BG697670 (1-663)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
DB 96 ATGGAAGCGCCCATCCAGTGTCTCTGGACCTGTGACCCACCCAGTTCGGCTGCAGC 155
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
DB 156 AATGGCTGCTGCATCGACAGTTCTCTGGAGTGTGACGACACCCCAACTGCCCGAGGCC 215
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 216 TCCGACGAGGCTGCTGTGAAAATAACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 275
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 276 TTCCCCAGTGACAAAGGCGACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGGC 335
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
DB 336 ATCCCGCGCTGGTACTACACCCCTTCAGCGACACTGCGCCGCTTTACCTATGGTGGT 395
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
DB 396 TGTATGGCAACAGAACAACTTTGAGGAAGAGCAGAGTGGCTCGAGTCTTGTGCGGCGC 455
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
DB 456 ATCTCCAGAGGATGTGTTGGCTGAGCGGGGAATCCCATTTCCAGCAGCAGGCTCT 515
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
DB 516 GTGGAGATGGCTGTGCGAGTGTCTCTGGTCACTGCTGATTTGGTGGTGGTAGCCATCTTG 575
QY 161 GlyTyrCysPhePheLysAsnGlnArgLys-AspPheHisGlyHisHisHisProPr 180
DB 576 GGTACTGCTTCTTCAGAACCCAGAGAAACCGGACTTCCAGGACACCATCATCAACGAGC 635
QY 180 oProThrProAlaSerSerThrValSer 189
DB 636 AACACCCCTGCGAGTCTCCACTGTCTCC 663


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RESULT 10
BX336602      1201 bp      mRNA      linear      EST 02-MAY-2003
LOCUS          BX336602 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION     Clone CS0DI030YE23 5-PRIME, mRNA sequence.
ACCESSION      BX336602
VERSION        BX336602.1 GI:30339518
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL       1 (bases 1 to 1201)
COMMENT       Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI030AC12QP1&cluster=7854.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DI030AC12QP1.
Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI030YE23"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/Note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
```

Alignment Scores:

Pred. No.:	8.67e-94	Length:	1201
Score:	1016.00	Matches:	181
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.45%	Mismatches:	0
Query Match:	87.06%	Indels:	0
DB:	13	Gaps:	0

us-09-935-390A-23 (1-206) x BX336602 (1-1201)

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QY      25  ileAspSerPheLeuGluCysAspThrProAsnCysProAspAlaSerAspGluAla 44
DB      65  ATCGACAGTTTCTGAGTGTGACGACACCCCACTGCCCCGACGCTCCGACGAGGCT 124
QY      45  AlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHisPheProSerAsp 64
DB      125 GCCTGTGAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTCCCGACGAC 184
QY      65  LysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSerIleProArgTrp 84
DB      185 AAAGGGCACTGGCTGGACCTGCCACACACAGGACCTTGCAGGAGAGCATCCCGCGCTGG 244
QY      85  TyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGlyCysTyrGlyAsn 104
DB      245 TACTACAACCCCTTCAGCGAACAACCTGCCCGCTTTACCTATGTTGTTATGGCAAC 304
QY      105 LysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGlyIleSerLysLys 124
DB      305 AAGAACAACCTTTGAGGAAGAGCAGCGAGTGCCTCGAGTCTTGTGCGGCGCATCTCCAAGAG 364
QY      125 AspValPheGlyLeuArgArgGluIleProIleProSerThrGlySerValGluMetAla 144
```

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Db      365 GATGTGTTGGCCTGAGCGGGAAATCCCATCCACACAGGCTTGTGGAGATGGCT 424
QY      145 ValAlaValPheIleuValIleCysIleValValValValAlaIleLeuGlyTyrCysPhe 164
DB      425 GTCCAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
QY      165 PheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisHisHisHisHisHisHis 184
DB      485 TTCAAGAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544
QY      185 SerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsnHisThrThrArg 204
DB      545 AGCTCCACTGCTCTCCACTACCGAGGACACGAGGACCTGGTCTATATACACACACCCCGG 604
QY      205 ProLeu 206
DB      605 CCCCCTC 610
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RESULT 11
BE794925
LOCUS BE794925 882 bp mRNA linear EST 20-SEP-2000
DEFINITION 601589675F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943699 5',
mRNA sequence.
ACCESSION BE794925
VERSION BE794925.1 GI:10216123
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL 1 (bases 1 to 882)
COMMENT NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: DCTP/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM99 row: f column: 20
High quality sequence stop: 766.
Location/Qualifiers
1..882
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3943699"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/Note="Organ: lung; Vector: pOTS7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Alignment Scores:

Pred. No.:	3.33e-93	Length:	882
Score:	1008.50	Matches:	184
Percent Similarity:	92.20%	Conservative:	5
Best Local Similarity:	89.76%	Mismatches:	11
Query Match:	86.42%	Indels:	5
DB:	10	Gaps:	2

ORIGIN


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/dev_stage="6 days neonate"
82.1605
/note="unnamed protein product; putative
serine protease inhibitor, Kunitz type 1
(MGD|MGI:138033)"
/codon_start=1
/protein_id="BAB30697.1"
/db_xref="GI:12856531"
/translation="MAGRRRLARASISAVGVWLLCALGLQATBAXLPSPAPLPGGAAC
LSRFTSGVPSFVLDTFASVNGATFLGSPPTARRGWDVRSCTTQNCNLALVELQPDG
GEDAISACFLNCLYEQNFVKFAPKEGPIYLTQELYSRVELTRGFGGSRIPRIW
MGIDLKVLQKPLVLEADNTDWHLLQDSDVRVERKRPPEVSLWGLKEGTYLFOLTR
TDSDDPESTANLTITVLTAQOTEDYCLASYKVGRCSPFRNYDYPKEQICKSFTFGG
CLGNKNYLRBEZCMLACKDVQGISPKRHHPVCSGSHATQFCNSGCCIDGFLBCDD
TPDCPDGDEATCEKYSYSGFDELQNIHFLSDKGYCAELPDTGFCKENIPRWYNNPFE
RCARFTYGGCYGNKNPFEHQCLSCRGISKDVFLRLREGSIPTVGSAEVAIAVFL
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2140..2145
/note="putative"
2155
/note="putative"
polyA_site
2155
/note="putative"
ORIGIN
Alignment Scores:
Pred. No.: 1.1e-91 Length: 2155
Score: 999.00 Matches: 173
Percent Similarity: 90.73% Conservative: 13
Best Local Similarity: 84.39% Mismatches: 19
Query Match: 85.60% Indels: 0
DB: 11 Gaps: 0
US-09-935-390A-23 (1-206) x AK017342 (1-2155)
QY 2 GluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSerAsn 21
Db 988 AAAAGGCACCATCCAGTGTCTCCGGCAGCTGCCATGCCACCCAGTTCCGCTGTAGCAAT 1047
QY 22 GlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAlaSer 41
Db 1048 GGCTGTGTATCGATGGCTTCTCGAGTGTGATGACACGCCAGACTGCCCTGTATGCTCC 1107
QY 42 AspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHisPhe 61
Db 1108 GACGAGGCCACCTGTGAAATAACACACGAGCGGCTTTGATGAGCTTCAGAAATATCCATTTC 1167
QY 62 ProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSerIle 81
Db 1168 CTCAGTGACAAAGGTACTGTGCAGAGCTGCCAGACACTGGTGTTCGAAAGAGACATC 1227
QY 82 ProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGlyCys 101
Db 1228 CCACGCTGTATTACAACCACTTCAGTGAACGCTGTGCCCGATTACCTATGTTGGTTC 1287
QY 102 TyrGlyAsnLysAsnAsnPheGluGluGluGlnGlnCysLeuGluSerCysArgGlyIle 121
Db 1288 TATGGGACAAAGAACAACTTTGAGGAGGAGACAGCAGTGTCTGAGTCTCGCGTGGCATC 1347
QY 122 SerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySerVal 141
Db 1348 TCCAAAGAGGATGTGTTGGTCTTCGAGGGAAGGCTCCATTCCCACTGTAGGCTCCGCT 1407
QY 142 GluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeuGly 161
Db 1408 GAGGTAGCTATTGCTGTATTTCTGGTCACTGTCATCATAGTGTCTTAACCATCTCTGGC 1467
QY 162 TyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProProPro 181
Db 1468 TACTGTTTCTTCAAGAACCAAGAAAGGAATTCCACAGTCCCTTGCACCCACCTCCC 1527
QY 182 ThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsnHis 201
Db 1528 ACACGAGCCAGCTCCACTGTTTCCACCAACAGAGGACACAGAGACCTGTCTATATCATC 1587
```

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QY 202 ThrThrArgProLeu 206
Db 1588 ACAACCCAGCCTCTC 1602
RESULT 13
BX369479 948 bp mRNA linear EST 08-MAY-2003
LOCUS BX369479 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
DEFINITION Homo sapiens cDNA clone CS0DJ014YC20 5-PRIME, mRNA sequence.
ACCESSION BX369479
VERSION BX369479.1 GI:30457815
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 948)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAF036ZG12_AF03456_1&cluster=7854.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0BAF036ZG12_AF03456_1.
FEATURES
Location/Qualifiers
1..948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ014YC20"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 2.34e-91 Length: 948
Score: 991.00 Matches: 190
Percent Similarity: 91.47% Conservative: 3
Best Local Similarity: 90.05% Mismatches: 12
Query Match: 84.92% Indels: 6
DB: 13 Gaps: 0
US-09-935-390A-23 (1-206) x BX369479 (1-948)
QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 294 ATGGAAGGCGCCATCCAGTGTCTCTGGCAGCTGTTCAGCCACCCAGTTCGGCTGCAGC 353
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db 354 AATGGCTGCTCATCGACAGTTTCTCTGGAGTGTGACGACACCCCACTGCCCGACGCC 413
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 414 TCCGACGAGGCTGCTGTGAAATAATACACGAGTGGCTTTGACGAGTCCAGGCGCATCAT 473
QY 61 PheProSerAspLysGlyHisCysValAsnLeuProAspThrGlyLeuCysLysGluSer 80
Db 474 TTCCCCAGTGACAAAGGCGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 533
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QY 81 ileProArgTrrpTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 534 ATCCCGGCTGGTACTACAAACCCCTTCAGCGAACACTGGCCCGCTTACCTATGGTGGT 593
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db 594 TGTATGGCAACAAGAACTTTGAGGAGACAGCAGTGCCTCGAGTCTTGTGCGGGC 653
QY 121 ileSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db 654 ATCTNCAAGAGGATGTGTTGGCTTGAGGCGGGAATCCCATTTCCAGCACAGGCTCT 713
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleVal-ValValValAlaIleLe 160
Db 714 GTGGAGATGGCTGCGCAGTGTCTCTGGTCACTGCTGATTTGGTGGTGGTAGCCATCTT 773
QY 160 uGlyTyrCysPhePheLysAsnGlnArgLysAspPheHis-GlyHisHisHisHisProp 180
Db 774 TGGTTACTGTTCTTCAAGACCAAGAGAAAGGACTTNCACGGGACACCACTCAACCAA 833
QY 180 roProThrProAlaSerSerThrValSerThrThr-GluAsp-ThrGluHis-LeuValT 199
Db 834 CAACCAACCTTGGCAGTTTCACTGTCTTTACTACCCGAGGACCACGGGACCCCTGGTCT 893
QY 199 yrAsnHisThr-ThrArgPro 205
Db 894 TTAACCAACACCCACCCGCGCC 914

RESULT 14
CF146773
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
889548
PUBMED
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Tim Ratliff
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
The following repetitive elements were found in this cDNA
sequence: 426-483, >(TGG)n#Simple_repeat (matched complement)
Seq primer: pyx-5.
Location/Qualifiers
1. .647
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30570529"
/tissue_type="CNCAP(3)T-225 cell line"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_MGC_210"
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/note="Organ: Prostate; Vector: pT7T3 Pac; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pT7T3 Pac vector. The library tag
sequence located between the Not I site and the polyA tail
is CCCAC. Tissue was provided by Tim Ratliff."

ORIGIN

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Alignment Scores:
Pred. No.: 7.46e-87 Length: 647
Score: 945.00 Matches: 173
Percent Similarity: 99.43% Conservative: 0
Best Local Similarity: 99.43% Mismatches: 1
Query Match: 80.98% Indels: 1
DB: 14 Gaps: 0

US-09-935-390A-23 (1-206) x CF146773 (1-647)

QY 33 AspThrProAsnCysProAspAlaSerAspGluAlaCysGlnLysTyrThrSerGly 52
Db 8 GACACCCCAACTGCCCGCAGCGCTCCGACGAGGCTGCTGTGAAAATA-ACGAGTGGC 66
QY 53 PheAspGluLeuGlnArgIleHisPheProSerAspLysGlyHisCysValAspLeuPro 72
Db 67 TTTGACGAGCTCCAGCGCATCCATTCCCCAGTGACAAAGGGCAGTGGTGGACCTGCCA 126
QY 73 AspThrGlyLeuCysLysGluSerIleProArgTrrpTyrAsnProPheSerGluHis 92
Db 127 GACACAGACTCTGCAAGGAGAGAGCATCCCGCGCTACTACAAACCCCTTCAGCGAACAC 186
QY 93 CysAlaArgPheThrTyrGlyGlyCysTyrGlyAsnLysAsnAsnPheGluGluGln 112
Db 187 TGGCCCGCTTTACCTATNGGTGGTGTATGTCACAAAGAACAACTTTGAGGAAGAGCAG 246
QY 113 GlnCysLeuGluSerCysArgGlyIleSerLysLysAspValPheGlyLeuArgGlu 132
Db 247 CAGTGCCTCGAGTCTTGTGCGGCGATCTCCAAGAGGATGTGTGGCTGAGCGGGAA 306
QY 133 IleProIleProSerThrGlySerValGluMetAlaValAlaValPheLeuValIleCys 152
Db 307 ATCCCCATTCACGACAGGCTCTGTGGAGATGGCTGTGCGAGTGTCTCTGCTCATCTGC 366
QY 153 IleValValValAlaIleLeuGlyTyrCysPhePheLysAsnGlnArgLysAspPhe 172
Db 367 ATTGTGGTGGTGGTAGCCATCTTGGGTACTGCTTCTTCAAGAACACAGAGAAAGGACTTC 426
QY 173 HisGlyHisHisHisHisProProProThrProAlaSerSerThrValSerThrGlu 192
Db 427 CACGGACACACACACACACACACACACACACACACACACACACACACACACACAC 486
QY 193 AspThrGluHisLeuValTyrAsnHisThrThrArgProLeu 206
Db 487 GACACGAGACCTGGTCTATATACCAACACACACACACACACACACACACACACAC 528
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RESULT 15
BX334952/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BX334952 1201 bp mRNA linear EST 01-MAY-2003
BX334952 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS01009YC11 3-PRIME, mRNA sequence.
BX334952
BX334952.1 GI:30310380
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI009AB06NP1&cluster=7854.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI009AB06NP1.

FEATURES
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/db_xref="taxon:9606"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 4.5e-81 Length: 1201
Score: 892.50 Matches: 168
Percent Similarity: 92.35% Conservative: 1
Best Local Similarity: 91.80% Mismatches: 13
Query Match: 76.48% Indels: 2
DB: 13 Gaps: 1

US-09-935-390A-23 (1-206) x BX334952 (1-1201)

Qy 24 CysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAlaSerAspGlu 43
Db 1190 TGCATCGACAKTTCTCTGRATK---KGAGACACCCCACTGCCCGMGCCTCGGACGAA 1134

Qy 44 AlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHisPheProSer 63
Db 1133 GCTGCCTKTGAAAAATACACGAGTGGCTTTGACGSAGTCCAGCGCATCCATTTCCCCAGT 1074

Qy 64 AspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSerIleProArg 83
Db 1073 GACAAAAGGGGCTGCGTGACACWTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGC 1014

Qy 84 TrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyCysTyrGly 103
Db 1013 TGGTACTACAACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTATGGC 954

Qy 104 AsnLysAsnAsnPheGluGluGluGlnCysLeuGluSerCysArgGlyIleSerLys 123
Db 953 AACAAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGCATCTCCAAG 894

Qy 124 LysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySerValGluMet 143
Db 893 AAGGATGTGTTTGGCCTGAGGCGGGAATCCCCATTCCAGACACAGGCTCTGTGGAGATG 834

Qy 144 AlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeuGlyTyrCys 163
Db 833 ST-GTCCAGTGTTCCTGGTCACTGTCATTGTGGTGGTGGTAGCCATCTTGGGTACTGC 775

Qy 164 PhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProProProThrPro 183
Db 774 TTCCTCAAGAACACAGAGAAAGGACTTCCACGGACACACACACACACCCACCCACCCCT 715

Qy 184 AlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsnHisThrThr 203
Db 714 GCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCMCCTGGTCTATATACACACACC 655

Qy 204 ArgProLeu 206
Db 654 CGGCCCTC 646

Search completed: April 22, 2004, 10:13:59
Job time : 2508 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 22, 2004, 08:23:19 ; Search time 413 Seconds
(without alignments)
2248.855 Million cell updates/sec

Title: US-09-935-390A-23
Perfect score: 1167
Sequence: 1 MERRHPVCSGTQPTQRC.....TVSITTEHLVYNHTTPL 206

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09935390/runat 20042004 144851 10444/app query.fasta_1.391
-DB=Published Applications NA -QFMT=fastap -SUPPIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09935390 @CGN 1 1 472 @runat 20042004 144851 10444
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

1	1167	100.0	1505	9	US-09-935-390A-4	Sequence 4, Appli
2	1167	100.0	1542	9	US-09-765-449-8	Sequence 8, Appli
3	1163	99.7	2482	9	US-09-742-201-1	Sequence 1, Appli
4	1163	99.7	2482	13	US-10-081-056-41	Sequence 41, Appli
5	1163	99.7	2482	13	US-10-245-752-9	Sequence 9, Appli
6	1163	99.7	2482	13	US-10-245-859-9	Sequence 9, Appli
7	1163	99.7	2482	13	US-10-211-858-11	Sequence 11, Appli
8	1163	99.7	2482	13	US-10-305-654-41	Sequence 41, Appli
9	1163	99.7	2482	15	US-10-245-103-9	Sequence 9, Appli
10	1163	99.7	2482	15	US-10-245-107-9	Sequence 9, Appli
11	1163	99.7	2482	15	US-10-245-143-9	Sequence 9, Appli
12	1163	99.7	2482	15	US-10-245-771-9	Sequence 9, Appli
13	1163	99.7	2482	15	US-10-245-851-9	Sequence 9, Appli
14	1163	99.7	2482	15	US-10-245-883-9	Sequence 9, Appli
15	1163	99.7	2482	15	US-10-237-535-9	Sequence 9, Appli
16	1163	99.7	2482	15	US-10-238-183-9	Sequence 9, Appli
17	1163	99.7	2482	15	US-10-238-283-9	Sequence 9, Appli
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20	1163	99.7	2482	15	US-10-245-147-9	Sequence 9, Appli
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22	1163	99.7	2482	15	US-10-245-739-9	Sequence 9, Appli
23	1163	99.7	2482	15	US-10-246-210-9	Sequence 9, Appli
24	1163	99.7	2482	15	US-10-239-196-9	Sequence 9, Appli
25	1163	99.7	2482	15	US-10-243-024-9	Sequence 9, Appli
26	1163	99.7	2482	15	US-10-243-409-9	Sequence 9, Appli
27	1163	99.7	2482	15	US-10-245-621-9	Sequence 9, Appli
28	1163	99.7	2482	15	US-10-245-880-9	Sequence 9, Appli
29	1163	99.7	2482	15	US-10-245-033-9	Sequence 9, Appli
30	1163	99.7	2482	15	US-10-243-095-9	Sequence 9, Appli
31	1163	99.7	2482	15	US-10-245-185-9	Sequence 9, Appli
32	1163	99.7	2482	15	US-10-245-427-9	Sequence 9, Appli
33	1163	99.7	2482	15	US-10-245-473-9	Sequence 9, Appli
34	1163	99.7	2482	15	US-10-245-770-9	Sequence 9, Appli
35	1163	99.7	2482	15	US-10-245-877-9	Sequence 9, Appli
36	1163	99.7	2482	15	US-10-246-976-9	Sequence 9, Appli
37	1163	99.7	2482	15	US-10-243-320-9	Sequence 9, Appli
38	1163	99.7	2482	15	US-10-242-743-9	Sequence 9, Appli
39	1163	99.7	2482	15	US-10-242-845-9	Sequence 9, Appli
40	1163	99.7	2482	15	US-10-223-085-41	Sequence 41, Appli
41	1163	99.7	2482	15	US-10-237-636-9	Sequence 9, Appli
42	1163	99.7	2482	15	US-10-238-325-9	Sequence 9, Appli
43	1163	99.7	2482	15	US-10-238-346-9	Sequence 9, Appli
44	1163	99.7	2482	15	US-10-238-411-9	Sequence 9, Appli
45	1163	99.7	2482	15	US-10-243-124-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-935-390A-4
; Sequence 4, Application US/09935390A
; Patent No. US20020076761A1
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
; Quianjin, Hu
; Garcia, Pablo
; Williams, Lewis T.
; Kothakota, Srinivas
; TITLE OF INVENTION: Secreted Human Proteins
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/935,390A
FILING DATE: 22-AUG-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/988,671
FILING DATE: 1997-12-11
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. R. Potter
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 1369.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2718
TELEFAX: (510) 655-3542
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-935-390A-4
Alignment Scores:
Pred. No.: 4.36e-145 Length: 1505
Score: 1167.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-935-390A-23 (1-206) x US-09-935-390A-4 (1-1505)
QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
171 ATGGAAGCGCCATCCAGTGTCTGTCACCTGTGACCCACCCAGTTCGGCTGCAGC 230
QY 21 AsnGlyCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
231 AATGGCTGCTGCATCGACAGTTTCTCGAGTGTGACGACACCCCACTGCCCGACGCC 290
QY 41 SerAspGluAlaAlaCysGluLysThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
291 TCCGACGAGGCTGCCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 350
QY 61 PheProSerAspIysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
351 TTCCCGACGCAAGGCGCACTCGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 410
QY 81 IleProArgTrpTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
411 ATCCCGCGCTGGTACTACAAACCCCTTCAGCGAACACTGCGCCCGCTTACCTATGGTGGT 470
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
471 TGTACGGCAACAGAACAACTTTGAGGAAGACGACGAGTGCCTCGAGTCTTGTGCGGGC 530
QY 121 IleSerLysLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer 140
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
531 ATCTCCAGAGGATGTGTTGGCTGAGCGGGAATCCCACTTCCAGCACAGGCTCT 590
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
591 GTGAGATGGCTGTGCGAGTGTCTCGTATCTGATGTTGGTGTGTTGGTGTGATCTTG 650
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
651 GGTACTGCTTCTTCCAGAACACAGAGAGGACTTCCAGGACACCCACCCACCCACCA 710
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 711 CCCACCCCTGCCAGTCCACTGTCTTCCACTACCGAGGACAGGACCTGTCTATAAC 770
QY 201 HistThrArgProLeu 206
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
771 CACACCACGCGGCCCTC 788
RESULT 2
US-09-765-449-8
; Sequence 8, Application US/09765449
; Patent No. US20020098537A1
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; KAWAGUCHI, Toshiya
; KITAMURA, Naomi
; MIYAZAWA, Keiji
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,449
; FILING DATE: 22-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,558
; FILING DATE: <Unknown>
; INFORMATION FOR SEQ ID NO: 8
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: MKN45
; (ix) FEATURES:
; SEQUENCE DESCRIPTION: SEQ ID NO: 8
US-09-765-449-8
Alignment Scores:
Pred. No.: 4.52e-145 Length: 1542
Score: 1167.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-935-390A-23 (1-206) x US-09-765-449-8 (1-1542)
QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
922 ATGGAAGCGCCATCCAGTGTGCTCTGGCACCTGTGACCCACCCAGTTCGGCTGCAGC 981
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
982 AATGGCTGCTGCATCGACAGTTTCTCGAGTGTGACGACACCCCACTGCCCGACGCC 1041
QY 41 SerAspGluAlaAlaCysGluLysThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
1042 TCCGACGAGGCTGCCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1101

QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1102 TTCCCAAGTACAAAGGCACTGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1161
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 1162 ATCCCGGCTGGTACTACAAACCCCTTCAGCGAACACTGCGCCGCTTTACCTATGTTGGT 1221
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGluGlnCysLeuGluSerCysArgGly 120
Db 1222 TGTTATGGCAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTTGTCGGCGC 1281
QY 121 IleSerLysLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer 140
Db 1282 ATCTCAAGAAGGATGTGTTGGCTGAGGCGGGAATCCCATTTCCAGCACAGGCTCT 1341
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db 1342 GTGGAGATGGCTGTCGAGTGTTCCTGGTCACTCTGCATTGTGGTGTAGCCATCTTG 1401
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 1402 GGTTACTGCTTCTTCAAGAACCCAGAGAAAGGACTTCCACGGACACCCACCCACCA 1461
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 1462 CCCACCCCTGCCAGCTCCACTGCTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1521
QY 201 HisThrThrArgProLeu 206
Db 1522 CACACCCACCGGCCCTC 1539

RESULT 3

US-09-742-201-1
; Sequence 1, Application US/09742201
; Patent No. US20020123091A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kirchhofer, Daniel K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: No. US20020123091A1 Inhibitor of Hepatocyte Growth Factor Activ
; TITLE OF INVENTION: for Use in Modulation of Angiogenesis and Cardiovascularization
; FILE REFERENCE: P1861RUS
; CURRENT APPLICATION NUMBER: US/09/742,201
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US00/06884
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 60/253,665
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-742-201-1

Alignment Scores:
Pred. No.: 3.12e-144 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
Gaps: 0

US-09-935-390A-23 (1-206) x US-09-742-201-1 (1-2482)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 1157 ATGGAAGGCGCCATCCAGTGTGCTCTGGCACCTGTGACCCACCCAGTTCGCTGCAGC 1216
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40

Db 1217 AATGGCTGCTGATGACAGATTTCCTGGAGTGTGACGACACCCCACTGCCCGACGCC 1276
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 1277 TCCGACGAGGCTGCTGTGAAAAATACACGACTGGCTTTTGACGAGCTCCAGCGCATCCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1337 TTCCCAAGTACAAAGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1396
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 1397 ATCCCGGCTGGTACTACAAACCCCTTCAGCGAACACTGCGCCGCTTTACCTATGTTGGT 1456
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGluGlnCysLeuGluSerCysArgGly 120
Db 1457 TGTTATGGCAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTTGTCGGCGC 1516
QY 121 IleSerLysLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer 140
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QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
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QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 1637 GGTTACTGCTTCTTCAAGAACCCAGAGAAAGGACTTCCACGGACACCCACCCACCA 1696
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Db 1697 CCCACCCCTGCCAGCTCCACTGCTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1756
QY 201 HisThrThrArgProLeu 206
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RESULT 4

US-10-081-056-41
; Sequence 41, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Maisters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C1
; CURRENT APPLICATION NUMBER: US/10/081,056
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25

;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: 2000-07-28
;; PRIOR APPLICATION NUMBER: US 60/222,695
;; PRIOR FILING DATE: 2000-08-02
;; PRIOR APPLICATION NUMBER: US 09/643,657
;; PRIOR FILING DATE: 2000-08-17
;; PRIOR APPLICATION NUMBER: PCT/US00/23522
;; PRIOR FILING DATE: 2000-08-23
;; PRIOR APPLICATION NUMBER: PCT/US00/23328
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: US 60/230,978
;; PRIOR FILING DATE: 2000-09-07
;; PRIOR APPLICATION NUMBER: US 60/000,000
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: US 09/664,610
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: US 09/665,350
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: US 60/242,922
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 09/709,238
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: PCT/US00/30952
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: PCT/US00/30873
;; PRIOR FILING DATE: 2000-11-10
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; PRIOR APPLICATION NUMBER: US 09/747,259
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/34956
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: US 09/767,609
;; PRIOR FILING DATE: 2001-01-22
;; PRIOR APPLICATION NUMBER: US 09/796,498
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: PCT/US01/06666
;; PRIOR FILING DATE: 2001-03-01
;; PRIOR APPLICATION NUMBER: US 09/802,706
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: US 09/808,689
;; PRIOR FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: US 09/816,744
;; PRIOR FILING DATE: 2001-03-22
;; PRIOR APPLICATION NUMBER: US 09/828,366
;; PRIOR FILING DATE: 2001-04-05
;; PRIOR APPLICATION NUMBER: US 09/854,208
;; PRIOR FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: US 09/854,280
;; PRIOR FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: US 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 09/866,034
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: PCT/US01/17092
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 09/870,574
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: PCT/US01/17443
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: PCT/US01/17800
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/00000
;; PRIOR FILING DATE: 2001-06-28
;; NUMBER OF SEQ ID NOS: 383
;; SEQ ID NO 41
;; LENGTH: 2482
;; TYPE: DNA
;; ORGANISM: Homosapiens

US-10-081-056-41
Alignment Scores:
Pred. No.: 3.12e-144 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 13 Gaps: 0
US-09-935-390A-23 (1-206) x US-10-081-056-41 (1-2482)
QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 1157 ATGGAAGGCGCCATCCAGTGTCTCTGGCACCTGTTCAGCCACCCAGTTCGGCTGCAGC 1216
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db 1217 AATGGCTGCTGCATCGACAGTTTCTTGGAGTGTGACGACACCCCACTGCCCCGACGCC 1276
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 1277 TCCGACGAGGCTGCTGTGAAAAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1337 TTCCCCAGTGCACAAAGGCGCACTGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1396
QY 81 IleProArgTTPTyTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 1397 ATCCCGCGCTGCTACTACAACTTTCAGCGAACAACACTGCGCCCGCTTACCTATGTGTGT 1456
QY 101 CysTyrGlyAsnLysAsnAsnAsnPheGluGluGluGlnCysLeuGluSerCysArgGly 120
Db 1457 TGTATGGCAACAAGAACAACTTTGAGGAAGAGCAGAGTGCCTCGAGTCTTGTGCGGCG 1516
QY 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db 1517 ATCTCCAAGAGGATGTTTGGCCTGAGCGGGAATCCCATTTCCAGACACAGGCTCT 1576
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db 1577 GTGGAGATGGCTGTACAGTGTCTCTGCTGTCATCTGTCATTTGTGGTGTGTAGCCATCTT 1636
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro 180
Db 1637 GGTACTGCTTCTTCAAGAACACAGAGAAGGACTTCCACGGACACCCACACCCACCA 1696
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 1697 CCCACCCCTGCCAGTCCACTGTCTCCACTACCGAGGACACGGGACACCTGCTCTATAAC 1756
QY 201 HisThrThrArgProLeu 206
Db 1757 CACACCACCCGCGCCCTC 1774
RESULT 5
US-10-245-752-9
; Sequence 9, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Pong, Sherman


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QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 1157 ATGGAAGGCGCCATCCAGTGTCTGGACCTGTCCAGCCACCCAGTTCGGCTGCAGC 1216
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db 1217 AATGGCTGCTGCATCGACAGTTTCTGGAGTGTGACGACACCCCACTTCGAGGAGC 1516
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 1277 TCCGACGAGGCTGCTGTGAAATAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1337 TTCCCCAGTGACAAAGGCGCACTGGTGGACCTGCCAGACACAGCACTCTGCAAGGAGC 1396
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 1397 ATCCCGGCTGTGTACTACACCCCTTCAGCGAACACTGGCCCGCTTTACCTATGGTGGT 1456
QY 101 CysTyrGlyAsnLysAsnAspPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db 1457 TGTATGGCAACAGAACAACTTTGAGGAAGAGCAGCAGTGGCTCGAGTCTTGTGCGGCG 1516
QY 121 IleSerLysLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer 140
Db 1517 ATCTCCAAAGAGGATGTGTTTGGCCCTGAGCGCGGAAATCCCAATCCAGCACAGCTCT 1576
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db 1577 GTGGAGATGGCTGTACAGTGTCTCGTCTCATCTGCTATGTGGTGTGGTATGCTTGTG 1636
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 1637 GGTACTGCTTCTCAAGAACCCAGAGAAAGGAGCTTCCACGAGACACCAACCCACCA 1696
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 1697 CCCACCCCTGCCAGCTCCACTGTCTCCACTACGAGGACACGAGCACCTGGTCTATAAC 1756
QY 201 HisThrThrArgProLeu 206
Db 1757 CACACCAACCCGCCCCCTC 1774

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RESULT 7

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US-10-211-858-11
; Sequence 11, Application US/10211858
; Publication No. US20030211096A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/211,858
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17

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; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 11
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-211-858-11

Alignment Scores:
Pred, No.: 3, 12e-144 Length: 2482
Score: 1163.00 Matches: 205
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 13 Gaps: 0

US-09-935-390A-23 (1-206) x US-10-211-858-11 (1-2482)

QY 1 MetGluArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 1157 ATGGAAGGCGCCATCCAGTGTCTCTGGACCTGTCCAGCCACCCAGTTCGGCTGCAGC 1216
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db 1217 AATGGCTGCTGCATCGACAGTTTCTGGAGTGTGACGACACCCCACTTCGAGGAGC 1276
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 1277 TCCGACGAGGCTGCTGTGAAATAATACAGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1337 TTCCCCAGTGACAAAGGCGCACTGGTGGACCTGCCAGACACAGCACTCTGCAAGGAGC 1396
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 1397 ATCCCGGCTGTGTACTACACCCCTTCAGCGAACACTGGCCCGCTTTACCTATGGTGGT 1456
QY 101 CysTyrGlyAsnLysAsnAspPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db 1457 TGTATGGCAACAGAACAACTTTGAGGAAGAGCAGCAGTGGCTCGAGTCTTGTGCGGCG 1516
QY 121 IleSerLysLysAspValPheGlyLeuArgGluIleProIleProSerThrGlySer 140
Db 1517 ATCTCCAAAGAGGATGTGTTTGGCCCTGAGCGCGGAAATCCCAATCCAGCACAGCTCT 1576
QY 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
Db 1577 GTGGAGATGGCTGTACAGTGTCTCGTCTCATCTGCTATGTGGTGTGGTATGCTTGTG 1636
QY 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 1637 GGTACTGCTTCTCAAGAACCCAGAGAAAGGAGCTTCCACGAGACACCAACCCACCA 1696
QY 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 1697 CCCACCCCTGCCAGCTCCACTGTCTCCACTACGAGGACACGAGCACCTGGTCTATAAC 1756
QY 201 HisThrThrArgProLeu 206

```



```

Db      1697 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGACACCTGGTCTATAAC 1756
Qy      201 HisThrThrArgProLeu 206
        |||||||
Db      1757 CACACCAACCCGGCCCCCTC 1774

RESULT 11
US-10-245-143-9
; Sequence 9, Application US/10245143
; Publication No. US20030068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C90
; CURRENT APPLICATION NUMBER: US/10/245,143
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO '9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-143-9

Alignment Scores:
Pred. No.:      3.12e-144      Length:      2482
Score:          1163.00      Matches:      205
Percent Similarity: 99.51%      Conservative: 0
Best Local Similarity: 99.51%      Mismatches: 1
Query Match:      99.66%      Indels:      0
DB:              15          Gaps:      0

US-09-935-390A-23 (1-206) x US-10-245-143-9 (1-2482)
Qy      1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
        |||||||
Db      1157 ATGGAAGGGCCCATCCAGTGTCTCTGGACCTGTTCAGCCACCCAGTTCGGCTGCAGC 1216

Qy      21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
        |||||||
Db      1217 AATGGCTGTGTCATCGACAGTTTCTCGAGTGTGACGACACCCCACTGCCCGACGCC 1276

```

```
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-771-9

Alignment Scores:
Pred. No.:      3.12e-144      Length:      2482
Score:          1163.00      Matches:      205
Percent Similarity: 99.51%      Conservative: 0
Best Local Similarity: 99.51%      Mismatches: 1
Query Match:     99.66%      Indels:      0
DB:              15      Gaps:        0

US-09-935-390A-23 (1-206) x US-10-245-771-9 (1-2482)

Qy      1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db      1157 ATGGAAGGCGCCATCCAGTGTCTCTGGCACCTGTCCAGCCACCCAGTTCGGCTGCAGC 1216

Qy      21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db      1217 AATGGCTGCTGCATCGACAGTTTCTCTGGAGTGTGACGACACCCCAACTGCCGCGATCCAT 1276

Qy      41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db      1277 TCCGACGAGGCTGCTGTGAAATAATACACGAGTGGCTTGACGAGCTCCAGCGCATCCAT 1336

Qy      61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db      1337 TTCCCCAGTGACAAAGGCGCACTCGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1396

Qy      81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgpPheThrTrpGlyGly 100
Db      1397 ATCCCGCGCTGGTACTACAAACCTTCAGCGAACACTGCGCCCGCTTTACCTATGCTGT 1456

Qy      101 CysTrpGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120
Db      1457 TGTTATGGCAACAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCCGCGC 1516

Qy      121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db      1517 ATCTCCAAAGAAGGATGTGTTGGCTGAGCGGGAAATCCCATTTCCAGCACAGGCTCT 1576

Qy      141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaAlaIleLeu 160
Db      1577 GTGGAGATGGCTGTACAGTGTTCCTGGTCACTGTGCTATGCTGCTGCTGCTGCTGCTG 1636

Qy      161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db      1637 GGTACTGCTTCTTCAAGAACCAAGAGAAAGGACTTCCACGGACACACCAACCCACCA 1696

Qy      181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db      1697 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACTGGTCTATAAC 1756

Qy      201 HistThrThrArgProLeu 206
Db      1757 CACACCACCGGCCCTC 1774

RESULT 13
US-10-245-851-9
; Sequence 9, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C93
; CURRENT APPLICATION NUMBER: US/10/245,851
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-851-9

Alignment Scores:
Pred. No.:      3.12e-144      Length:      2482
Score:          1163.00      Matches:      205
Percent Similarity: 99.51%      Conservative: 0
Best Local Similarity: 99.51%      Mismatches: 1
Query Match:     99.66%      Indels:      0
DB:              15      Gaps:        0

US-09-935-390A-23 (1-206) x US-10-245-851-9 (1-2482)

Qy      1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db      1157 ATGGAAGGCGCCATCCAGTGTCTCTGGCACCTGTCCAGCCACCCAGTTCGGCTGCAGC 1216

Qy      21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db      1217 AATGGCTGCTGCATCGACAGTTTCTCTGGAGTGTGACGACACCCCAACTGCCGCGATCCAT 1276

Qy      41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db      1277 TCCGACGAGGCTGCTGTGAAATAATACACGAGTGGCTTGACGAGCTCCAGCGCATCCAT 1336

Qy      61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db      1337 TTCCCCAGTGACAAAGGCGCACTCGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1396

Qy      81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgpPheThrTrpGlyGly 100
Db      1397 ATCCCGCGCTGGTACTACAAACCTTCAGCGAACACTGCGCCCGCTTTACCTATGCTGT 1456
```


Db 1397 ATCCCGCGCTGGTACTACAAACCCCTTCAGCGAACAACACTGGCGCCGCTTTACCTATGGTGGT 1456
Qy 101 CysTyrGlyAsnLysAsnLysPheGluGluGluGlnCysLeuGluSerCysArgGly 120
Db 1457 TGTATGGCAACAAGAACACTTTGAGGAAGAGCAGAGTGCCTCGAGTCTTGTGGCGGC 1516
Qy 121 IleSerLysLysAspValPheGlyLeuArgArgGluLeuProIleProSerThrGlySer 140
Db 1517 ATCTCAAGAAGGATGTGTGGCCTGAGCGCGGAAATCCCATTCACAGCAGGCTCT 1576
Qy 141 ValGluMetAlaValAlaValPheLeuValIleCysLeuValValValValAlaLeu 160
Db 1577 GTGGAGATGGCTGTACAGTGTTCCTGGTCATCTGCAATGTGGTGGTAGCCATCTTG 1636
Qy 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 1637 GGTACTGCTTCTTCAAGAACAGAGAAAGGACTTCCACGGACACCCACCCACCA 1696
Qy 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 1697 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1756
Qy 201 HisThrThrArgProLeu 206
Db 1757 CACACCACCGCGCCCTC 1774

RESULT 14
US-10-245-883-9
; Sequence 9, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C70
; CURRENT APPLICATION NUMBER: US/10/245,883
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 9
; LENGTH: 2482
; TYPE: DNA

; ORGANISM: Homo Sapien
US-10-245-883-9
Alignment Scores: 3,12e-144 Length: 2482
Pred. No.: 1163.00 Matches: 205
Score: 1163.00
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 99.66% Indels: 0
DB: 15 Gaps: 0
US-09-935-390A-23 (1-206) x US-10-245-883-9 (1-2482)
Qy 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 1157 ATGGAAGCGGCATCCAGTGTCTCTGGCACCTGTGAGCCACCCAGTCCGCTGCAGC 1216
Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
Db 1217 AATGGCTGTGCATCGACAGTTTCTTGGAGTGTGACGACACCCCACTGCCCGAGGCC 1276
Qy 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 1277 TCCGACGAGGCTGCCTGTGAAAAATACAGAGTGGCTTTGACGAGTCCAGCGCATCCAT 1336
Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 1337 TTCCCGAGTGACAAAGGCACCTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1396
Qy 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 1397 ATCCCGCGCTGGTACTACACCCCTTTCAGCGAAACACTGCGCCCGCTTTACCTATGGTGGT 1456
Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnCysLeuGluSerCysArgGly 120
Db 1457 TGTATGGCAACAAGAACACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGGCGGC 1516
Qy 121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
Db 1517 ATCTCAAGAGGATGTGTGGCTTGGCTGAGCGGGAATCCCATTTCCAGACACAGGCTCT 1576
Qy 141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaLeu 160
Db 1577 GTGGAGATGGCTGTACAGTGTTCCTGGTCACTGTCATTTGTGGTGGTAGCCATCTTG 1636
Qy 161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
Db 1637 GGTACTGCTTCTTCAAGAACAGAGAAAGGACTTCCACGGACACCCACCCACCA 1696
Qy 181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
Db 1697 CCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1756
Qy 201 HisThrThrArgProLeu 206
Db 1757 CACACCACCGCGCCCTC 1774
RESULT 15
US-10-237-535-9
; Sequence 9, Application US/10237535
; Publication No. US20030073188A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630RIC3
CURRENT APPLICATION NUMBER: US/10/237,535
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/133459
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/135725
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135729
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/140653
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144732
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
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PRIOR FILING DATE: 1999-07-20
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PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
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PRIOR APPLICATION NUMBER: 60/170362
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/177118
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/198587
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
PRIOR FILING DATE: 2000-04-25
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PRIOR FILING DATE: 2000-05-23
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PRIOR APPLICATION NUMBER: 60/218371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/229896
PRIOR FILING DATE: 2000-09-01
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PRIOR FILING DATE: 2001-03-09
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PRIOR FILING DATE: 2001-04-04
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PRIOR FILING DATE: 2001-05-09

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1517 ATCTCCAGAAGGATGTGTTTGGCCCTGAGCGCGGAATCCCCATTCAGCAGGCTCT 1576
141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu 160
1577 GTGGAGATGGCTGTACAGTGTTCCTGTCATCTGCATTGTGTGGTGTAGCCATCTTG 1636
161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
1637 GGTTACTGCTTCTTCAAGAACCCAGAGAAAGGACTTCCACGGACACCCACCACCA 1696
181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
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Job time : 422 secs

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PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
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PRIOR FILING DATE: 2001-06-01
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/924419
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/927796
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/931836
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 10/001054
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/081056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 10/119480
PRIOR FILING DATE: 2002-04-09

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US-09-935-390A-23 (1-206) x US-10-237-535-9 (1-2482)

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1217 AATGGCTGCTGCATCGACAGTTTCTGGAGTGTGACGACACCCCACTGCCCGGACGCC 1276
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
1277 TCCGAGAGGCTGCCCTGTGAAATAACAGAGTGGCTTGACGAGCTCCAGCGCATCCAT 1336
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
1337 TTCCCGAGTGACAAAGGGCACTGGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1396
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
1397 ATCCCGGCTGGTACTACAAACCCCTTCAGCGAACACTGCGCCGCTTTACCTATGTTGT 1456
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly 120

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 22, 2004, 08:12:09 ; Search time 78 Seconds
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1167	100.0	1542	US-09-765-449-8	Sequence 8, Appli
3	1167	100.0	1870	US-09-071-709-6	Sequence 6, Appli
C 4	647	55.4	816	US-09-020-956-14	Sequence 14, Appli
C 5	647	55.4	816	US-09-030-607-14	Sequence 14, Appli
C 6	647	55.4	816	US-09-439-313-14	Sequence 14, Appli
C 7	647	55.4	816	US-09-352-616A-14	Sequence 14, Appli
C 8	647	55.4	816	US-09-232-149A-14	Sequence 14, Appli
C 9	647	55.4	816	US-09-159-812-14	Sequence 14, Appli
C 10	647	55.4	816	US-09-636-215-14	Sequence 14, Appli
C 11	647	55.4	816	US-09-685-166A-14	Sequence 14, Appli
C 12	647	55.4	816	US-09-115-453-14	Sequence 14, Appli

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C 21	572	49.0	760	4	US-09-685-166A-37	Sequence 37, Appli
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C 37	173	14.8	759	2	US-08-974-196-4	Sequence 4, Appli
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C 39	173	14.8	1610	3	US-09-013-896A-1	Sequence 1, Appli
C 40	173	14.8	1610	4	US-09-127-948-1	Sequence 1, Appli
C 41	154.5	13.2	979	1	US-08-147-710-1	Sequence 1, Appli
C 42	154.5	13.2	979	1	US-08-458-090-1	Sequence 1, Appli
C 43	154.5	13.2	979	2	US-08-457-887-1	Sequence 1, Appli
C 44	154.5	13.2	979	4	US-09-016-434-1378	Sequence 1378, Ap
C 45	154.5	13.2	979	4	US-09-904-621-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-685-558A-8
; Sequence 8, Application US/08685558A
; Patent No. 6225081
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; APPLICANT: MIYAZAWA, Keiji
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEARS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,558A
; FILING DATE: 24-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JPA Hei 7-187135
; FILING DATE: 24-JUL-1995
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA
 ANTI-SENSE: no
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 STRAIN: MKN45
 FEATURE:

NAME/KEY: coding sequence
 LOCATION: 1 to 1542
 IDENTIFICATION METHOD: by experiment
 NAME/KEY: signal peptide
 LOCATION: 1 to 105
 IDENTIFICATION METHOD: by experiment
 NAME/KEY: mature peptide
 LOCATION: 106 to 1542
 IDENTIFICATION METHOD: by experiment

US-08-685-558A-8

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 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

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QY	21	AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla	40
DB	982	AATGGCTGCTGCATCGACAGTTCTGGAGTGTGACGACACCCCACTGCCCGACGCC	1041
QY	41	SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis	60
DB	1042	TCCGACGAGGCTGCCTGTGAAATAATACAGAGTGGCTTTCAGGAGCTCCAGCGCATCCAT	1101
QY	61	PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer	80
DB	1102	TTCCCGAGTGACAAAGGCGCACTGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC	1161
QY	81	IleProArgTrpTyrTrpAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly	100
DB	1162	ATCCCGCGCTGGTACTACACCCCTTCAGCGAACACTGGCGCCGCTTTACTATGTTGGT	1221
QY	101	CysTyrGlyAsnLysAsnAsnGluGluGlnGlnCysLeuGluSerCysArgGly	120
DB	1222	TGTTATGGCAACAGAACACTTTCAGGAGAGCAGCAGTGCTCGAGTCTGTGCGGC	1281
QY	121	IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer	140
DB	1282	ATCTCCAAGAGGATGTGTTGGCTGAGCGCGGAATCCCATTTCCAGCACAGGCTCT	1341
QY	141	ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu	160
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QY	181	ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn	200
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QY	201	HisThrThrArgProLeu	206
DB	1522	CACACACCCGCGCCCTC	1539

RESULT 2

US-09-765-449-8

Sequence 8, Application US/09765449
 Patent No. 6465622
 GENERAL INFORMATION:
 APPLICANT: SHIMOMURA, Takeshi
 KAWAGUCHI, Toshiya
 KITAMURA, Naomi
 MIYAZAWA, Keiji
 TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
 AND METHOD OF PRODUCING THE PROTEIN
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09765,449
 FILING DATE: 22-Jan-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/685,558
 FILING DATE: <Unknown>
 INFORMATION FOR SEQ ID NO: 8
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1542 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ANTI-SENSE: no
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 STRAIN: MKN45
 (ix) FEATURES:
 SEQUENCE DESCRIPTION: SEQ ID NO: 8
 US-09-765-449-8

Alignment Scores:
 Pred. No.: 4.59e-119 Length: 1542
 Score: 1167.00 Matches: 206
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

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QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
DB 982 AATGGCTGCTGCATCGACAGTTCTGGAGTGTGACGACACCCCACTGCCCGACGCC 1041
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
DB 1042 TCCGACGAGGCTGCCTGTGAAATAATACAGAGTGGCTTTCAGGAGCTCCAGCGCATCCAT 1101
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
DB 1102 TTCCCGAGTGACAAAGGCGCACTGGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 1161
QY 81 IleProArgTrpTyrTrpAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
DB 1162 ATCCCGCGCTGGTACTACACCCCTTCAGCGAACACTGGCGCCGCTTTACTATGTTGGT 1221

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Dd	1222	TGTTATGGCAACAAGAAACAACTTTTGAGGAAGAGCAGTCCTCGAGTCTTGTGCGGC	1281
Cy	121	IleSerLysLysaspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer	140
Dd	1282	ATCTCCAAGAAGGATGTGTTTGGCCGTGAGCGGGGAATCCCATTCCACGACACAGGCTCT	1341
Cy	141	valGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu	160
Dd	1342	GTTGAGATGGCTGTGGCAGTGTTCCTGGTCATCTGCAATGTGGTGGTAGCCACTTG	1401
Cy	161	GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro	180
Dd	1402	GETTACTGCTTCTCAAGAACCCAGAGAAAGGACTTCCACGGACACCACCACCCACCA	1461
Cy	181	ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn	200
Dd	1462	CCCCCCCCCTGCCAGCTCCACTGTCTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC	1521
Cy	201	HisThrThrArgProLeu	206
Dd	1522	CACACCACCCGGCCCCCTC	1539

RESULT 3

US-09-071-709-6
Sequence 6, Application US/09071709
Patent No. 6171790
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,709
FILING DATE: Filed Herewith

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Pred. NO.:			

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QY	21	AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla	40
DB	620	AATGGCTGCTGCATCGACAGATTCTCTGGAGTGTGACGACACCCCACTGCCCGCAGGCC	679
QY	41	SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis	60
DB	680	TCCGACGAGGCTGGCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT	739
QY	61	PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer	80
DB	740	TTCCCCAGTGACAAAGGGCAC TGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC	799
QY	81	IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly	100
DB	800	ATCCCGCGCTGGTACTACAAACCCCTTCAGCGAACAACCTGCGCCCGCTTACCTATGGTGGT	859
QY	101	CysTyrGlyAsnLysAsnAsnPheGluGluGlnGlnCysLeuGluSerCysArgGly	120
DB	860	TGTTATGGCAACAAGAACAACTTTGAGGAAGACAGCAGTGCCCTCGAGTCTTGTGCGCGGC	919
QY	121	IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer	140
DB	920	ATCTCCAAAGAGGATGTGTTGGCCCTGAGGCGGGAAATCCCCATTCCCGACACAGGCTCT	979
QY	141	ValGluMetAlaValAlaValPheLeuValIleCysIleValValValAlaIleLeu	160
DB	980	GTGGAGATGGCTGTGCGCAGTGTTCCTGGTCACTCTGCATTGTGGTGGTAGCCATCTTG	1039
QY	161	GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro	180
DB	1040	GGTTACTGCTTCTTCAAGAACCCAGAGAAAGGACTTCCACGGACACCCACCACCCACCA	1099
QY	181	ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn	200
DB	1100	CCCAACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTTGGTCTATAAC	1159
QY	201	HisThrThrArgProLeu	206
DB	1160	CACACCAACCGGCCCTC	1177

88SIT,T 4

US-09-020-956-14/c
Sequence 14, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-020-956-14

Alignment Scores:
Pred. No.: 3.55e-62 Length: 816
Score: 647.00 Matches: 109
Percent Similarity: 99.10% Conservative: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 55.44% Indels: 0
DB: 3 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-020-956-14 (1-816)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 335 ATGGAAGGGCGCCATCCAGTGTCTCTGGACNTGTCCAGCCACCCAGTTCCGCTGCAGC 276
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 275 AATGGCTGCTGCATNGACAGTTTCTCTGGAGTGTGAAGACACCCCACTGCCCGACGGC 216
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 215 TCGGACGAGGCTGCTGTGAAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 156
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 155 TTCCCCAGTGACAAAGGCGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 96
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 95 ATCCCGCGCTGGTACTACAAACCCCTTCAGCGAACAACCTGCGCCCGCTTTACCTATGGTGGT 36
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGlu 111
Db 35 TGTTATGGCAACAAGAACCACTTTGAGGAAGAG 3

RESULT 5
US-09-030-607-14/c
; Sequence 14, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-030-607-14

Alignment Scores:
Pred. No.: 3.55e-62 Length: 816
Score: 647.00 Matches: 109
Percent Similarity: 99.10% Conservative: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 55.44% Indels: 0
DB: 3 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-030-607-14 (1-816)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 335 ATGGAAGGGCGCCATCCAGTGTCTCTGGACNTGTCCAGCCACCCAGTTCCGCTGCAGC 276
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 275 AATGGCTGCTGCATNGACAGTTTCTCTGGAGTGTGAAGACACCCCACTGCCCGACGGC 216
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 215 TCGGACGAGGCTGCTGTGAAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 156
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 155 TTCCCCAGTGACAAAGGCGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 96
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 95 ATCCCGCGCTGGTACTACAAACCCCTTCAGCGAACAACCTGCGCCCGCTTTACCTATGGTGGT 36
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGlu 111
Db 35 TGTTATGGCAACAAGAACCACTTTGAGGAAGAG 3

RESULT 6
US-09-439-313-14/c
; Sequence 14, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

```
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-14

Alignment Scores:
Pred. No.: 3.55e-62 Length: 816
Score: 647.00 Matches: 109
Percent Similarity: 99.10% Conservative: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 55.44% Indels: 0
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-439-313-14 (1-816)

Qy 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 335 ATGGAAGGGGCCATCCAGTGTGCTGTGGACNTGTGAGACACCCCACTGCCCCGAGC 276

Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 275 AATGGCTGCTGCATNGACAGTTTCTGTGAGTGTGAAGACACCCCACTGCCCCGAGC 216

Qy 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 215 TCGGACGAGGCTGCTGTGAAAATAACAGAGTGGCTTTGACGAGCTCCAGGCGATCCAT 156

Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 155 TTCCCAAGTACAAAGGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 96

Qy 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 95 ATCCCGCGCTGTACTACAAACCCCTTCAGCGAACAACACTGCGCCCGCTTACCTATGTTGGT 36

Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGlu 111
Db 35 TGTATGGCAACAAGAACAACTTTGAGGAAGAG 3

RESULT 7
US-09-352-616A-14/c
; Sequence 14, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
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; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-14

Alignment Scores:
Pred. No.: 3.55e-62 Length: 816
Score: 647.00 Matches: 109
Percent Similarity: 99.10% Conservative: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 55.44% Indels: 0
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-352-616A-14 (1-816)

Qy 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 335 ATGGAAGGGGCCATCCAGTGTGCTGTGGACNTGTGAGACACCCCACTGCCCCGAGC 276

Qy 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 275 AATGGCTGCTGCATNGACAGTTTCTGTGAGTGTGAAGACACCCCACTGCCCCGAGC 216

Qy 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 215 TCGGACGAGGCTGCTGTGAAAATAACAGAGTGGCTTTGACGAGCTCCAGGCGATCCAT 156

Qy 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 155 TTCCCAAGTACAAAGGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 96

Qy 81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 95 ATCCCGCGCTGTACTACAAACCCCTTCAGCGAACAACACTGCGCCCGCTTACCTATGTTGGT 36

Qy 101 CysTyrGlyAsnLysAsnAsnPheGluGlu 111
Db 35 TGTATGGCAACAAGAACAACTTTGAGGAAGAG 3

RESULT 8
US-09-232-149A-14/c
; Sequence 14, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-14

Alignment Scores:
Pred. No.: 3.55e-62 Length: 816
Score: 647.00 Matches: 109
Percent Similarity: 99.10% Conservative: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 55.44% Indels: 0
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-232-149A-14 (1-816)
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QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 335 ATGGAAGGCGCCATCCAGTGTCTCTGGACNTGTCAGCCACCCAGTTCGGCTGCAGC 276
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 275 AATGGCTGCTGCATNGACAGTTTCTTGGAGTGTGAAGACACCCCACTGCCCGACGCG 216
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 215 TCGGACGAGGCTGCCTGTGAAAATAACACGAGTGTTCAGGAGTCCAGCGCATCCAT 156
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 155 TTCCCCAGTGACAAAAGGCACTCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 96
QY 81 IleProArgTyrTyrAsnPropheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 95 ATCCCGCGCTGGTACTACAAACCCCTTCAGCGAACAACCTGGCGCCGCTTTACCTATGGTGGT 36
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlu 111
Db 35 TGTATGGCAACAAGAACAACTTTGAGGAAGAG 3
RESULT 9
US-09-159-812-14/c
; Sequence 14, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A,T,C or G
US-09-159-812-14
Alignment Scores:
Pred. No.: 3.55e-62 Length: 816
Score: 647.00 Matches: 109
Percent Similarity: 99.10% Conservative: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 55.44% Indels: 0
DB: 4 Gaps: 0
US-09-935-390A-23 (1-206) x US-09-159-812-14 (1-816)
QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 335 ATGGAAGGCGCCATCCAGTGTCTCTGGACNTGTCAGCCACCCAGTTCGGCTGCAGC 276
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 275 AATGGCTGCTGCATNGACAGTTTCTTGGAGTGTGAAGACACCCCACTGCCCGACGCG 216
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 215 TCGGACGAGGCTGCCTGTGAAAATAACACGAGTGTTCAGGAGTCCAGCGCATCCAT 156
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 155 TTCCCCAGTGACAAAAGGCACTCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 96

QY 81 IleProArgTyrTyrAsnPropheSerGluHisCysAlaArgPheThrTyrGlyGly 100
Db 95 ATCCCGCGCTGGTACTACAAACCCCTTCAGCGAACAACCTGGCGCCGCTTTACCTATGGTGGT 36
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGluGlu 111
Db 35 TGTATGGCAACAAGAACAACTTTGAGGAAGAG 3
RESULT 10
US-09-636-215-14/c
; Sequence 14, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A,T,C or G
US-09-636-215-14
Alignment Scores:
Pred. No.: 3.55e-62 Length: 816
Score: 647.00 Matches: 109
Percent Similarity: 99.10% Conservative: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 55.44% Indels: 0
DB: 4 Gaps: 0
US-09-935-390A-23 (1-206) x US-09-636-215-14 (1-816)
QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
Db 335 ATGGAAGGCGCCATCCAGTGTCTCTGGACNTGTCAGCCACCCAGTTCGGCTGCAGC 276
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
Db 275 AATGGCTGCTGCATNGACAGTTTCTTGGAGTGTGAAGACACCCCACTGCCCGACGCG 216
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
Db 215 TCGGACGAGGCTGCCTGTGAAAATAACACGAGTGTTCAGGAGTCCAGCGCATCCAT 156
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
Db 155 TTCCCCAGTGACAAAAGGCACTCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 96

[illegible]

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RESULT 11
US-09-685-166A-14/c
; Sequence 14, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(816)
; OTHER INFORMATION: n = A,T,C or G
US-09-685-166A-14

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Alignment Scores:
Pred. No.:      3.55e-62
Score:          647.00
Length:         816
Matches:        109
Percent Similarity: 99.10%
Conservative:   1
Best Local Similarity: 98.20%
Mismatch:       1
Query Match:    0
Indels:         0
DB:             4
Gaps:           0

US-09-9315-390A-23 (1-206) x US-09-685-166A-14 (1-816)

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Qy	1	MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer	20
Db	335	ATGGAAGGCGCCATCCAGTGTGCTCTGGCACTGTGACCCACCCAGTTCGGCTGCAGC	276
Qy	21	AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla	40
Db	275	AATGGCTGCTGCATNACAGTTTCCTGGAGTGTGAAGACACCCCCAACTGCCCCGACGCG	216
Qy	41	SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis	60
Db	215	TCGGACGAGGCTGCCTGTGAAAAATACACGAGTGGCTTTGACGAGTCCAGCGCATCCAT	156
Qy	61	PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer	80
Db	155	TTCCCCAGTGCACAAAGGGCACTGCTGGACCTGCCAGACACAGGACTCTGCAGGAGAGC	96

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Qy      81   ileProArgTnpTyTyAsnPropheSerGluHisCysAlaAArgPheThrTyGlyGly 100
Db      95   ATCCCGCGTGCTACTACAAACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGT 36
Qy     101   CysTyGlyAsnLysAsnAsnPheGluGluGlu 111
Db     35   TGTATTGGCAACAAGAACAACACTTTGAGGAAGAG 3
RESULT 12
US-09-115-453-14/c
; Sequence 14, Application US/09115453B
; Patent No. 6657056
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(816)
; OTHER INFORMATION: n = A,T,C or G
US-09-115-453-14
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Alignment Scores:	
Pred. No.:	3-55e-62
Score:	647.00
Percent Similarity:	99.10%
Best Local Similarity:	98.20%
Query Match:	55.44%
DB:	4
Length:	816
Matches:	109
Conservative:	1
Mismatches:	1
Indels:	0
Gaps:	0

```

US-09-935-390A-23 (1-206) x US-09-115-453-14 (1-816)

QY      1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
        |||||
DB    335 ATGGAAAGGCCCATCCAGTGTGCTCTGGCACNTGTTCAGCCCCACCCAGTTCGCCTGCAGC 276

QY      21 AsnGlyCysCysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAla 40
        |||||
DB    275 AATGGCTGCTGCATNGACAGTTTCCTGGAGTGTAAGACACCCCACAACACTGCCCCCGACGCG 216

QY      41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
        |||||
DB    215 TCGGACGAGGCTGCCTGTGAATAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 156

QY      61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
        |||||
DB    155 TTCCCCAGTGTACAAAGGCACTGCGTGGACCTGCCAGACACACAGGACTCTGCCAAGGAGAGC 96

QY      81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
        |||||
DB    95 ATCCCGCGCTGGTACTACAAACCCTTCAGCGAACACTCGCGCCGCGCTTTACCTATGGTGGT 36

QY     101 CysTyrGlyAsnLysAsnAsnPheGluGlu 111
        |||||
DB    35 TGTTATGGCAACACAGAACAACTTTGAGGAAGAG 3

```

RESULT 13
US-09-688-489-14/c
; Sequence 14, Application US/09688489
; Patent No. 6663377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427D2
CURRENT APPLICATION NUMBER: US/09/688,489
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 816
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(816)
OTHER INFORMATION: n = A,T,C or G

Alignment Scores:
Pred. No.: 3.55e-62 Length: 816
Score: 647.00 Matches: 109
Percent Similarity: 99.10% Conservatives: 1
Best Local Similarity: 98.20% Mismatches: 1
Query Match: 55.44% Indels: 0
DB: 4 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-688-489-14 (1-816)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
335 ATGGAAGGGCCCATCCAGTGTCTCTGGACNTGTGAGCCACCCAGTTCGGCTGCAGC 276
QY 21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
275 AATGGCTGCTGCATNGACAGTTCTCTGGAGTGTGAGACACCCCACTGCCCGACGCG 216
QY 41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
215 TCGACGAGGCTGCCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 156
QY 61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
155 TTCCCCAGTGACAAAGGCGCTGCGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGC 96
QY 81 IleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
95 ATCCCGCGCTGGTACTACACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGT 36
QY 101 CysTyrGlyAsnLysAsnAsnPheGluGlu 111
DB 35 TGTATGGCAACAAGAACAACTTTGAGGAAGAG 3

RESULT 14
US-09-020-956-37/c
Sequence 37, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-020-956-37

Alignment Scores:
Pred. No.: 5.85e-54 Length: 760
Score: 572.00 Matches: 103
Percent Similarity: 92.92% Conservatives: 2
Best Local Similarity: 91.15% Mismatches: 7
Query Match: 49.01% Indels: 2
DB: 3 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-020-956-37 (1-760)

QY 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
341 ATGGAAGGGCC-NATCCAGTGTGTCTGGACCTGTGAGCCACCCAGTTCGGCTGCAGC 283
QY 21 AsnGlyCys-CysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAl 40
282 AATGGCTGNTGNTATCGACAGTTTAGTGGAGTGTGACGACACCCCACTGCCCGGANGC 223
QY 40 aSerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHi 60
222 TTCGGAGGAGGCTGCTGTGAAAAATACACGAGTGGTNGACGAGCTCCAGCGCATCCA 163
QY 60 spheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSe 80
162 TTTCCCGAGTGACAAAGGGCATTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAG 103
QY 80 rIleProArgTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
102 CATCCCGCGCTGGTACTACACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGG 43
QY 100 YCysTyrGlyAsnLysAsnAsnPheGluGluGluGln 112
42 TTGTTATGGCAACAAGAACAACTTTGAGGAAGAGAG 6

RESULT 15
US-09-030-607-37/c
Sequence 37, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillion, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-030-607-37

Alignment Scores:
Pred. No.: 5.85e-54 Length: 760
Score: 572.00 Matches: 103
Percent Similarity: 92.92% Conservative: 2
Best Local Similarity: 91.15% Mismatches: 7
Query Match: 49.01% Indels: 2
DB: 3 Gaps: 0

US-09-935-390A-23 (1-206) x US-09-030-607-37 (1-760)

Qy	1	MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer	20
Db	341	ATGGAAGGCC-NATCCAGTGTGTCTGGCACCTGTCCGCCACCAGTTCGGTGCAGC	283
Qy	21	AsnGlyCys-CysIleAspSerPheLeuGluCysAspThrProAsnCysProAspAl	40
Db	282	AATGGGCTGNTGNATCGACAGTTTAGTGGAGTGTGACGACACCCCACTGCCCGGANGC	223
Qy	40	aSerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHi	60
Db	222	TTCCGAGGAGGCTGCTGTGAAAATACACGAGTGGTTNGAGAGCTCCAGCGCATCCA	163
Qy	60	sPheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSe	80
Db	162	TTTCCCAAGTGACAAAGGGCATTTGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAG	103
Qy	80	rIleProArgTyrTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGl	100
Db	102	CATCCCGCGCTGGTACTACACCCCTTCAGCGAACACTGCGCGCGCTTTACCTATGGTGG	43
Qy	100	yCysTyrGlyAsnLysAsnAsnPheGluGluGln	112
Db	42	TTGTTATGGCAACAAGAACAACTTTGAGGAAGAGCAG	6

Search completed: April 22, 2004, 10:15:22
Job time : 82 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2004, 04:43:13 ; Search time 123 Seconds
(without alignments)
6790.253 Million cell updates/sec

Title: US-09-935-390A-4
Perfect score: 1505
Sequence: 1 GAATTCGGCAGGAGGAGCAG.....AAAAAAGTCTGCGCGCGC 1505

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB ID	Description
		Match	Length		
1	1458.6	96.9	1870	3	US-09-071-709-6 Sequence 6, Appli
2	667.4	44.3	1542	3	US-08-685-558A-8 Sequence 8, Appli
3	667.4	44.3	1542	4	US-09-765-449-8 Sequence 8, Appli
C 4	413.4	27.5	816	3	US-09-020-956-14 Sequence 14, Appli
C 5	413.4	27.5	816	3	US-09-030-607-14 Sequence 14, Appli
C 6	413.4	27.5	816	4	US-09-439-313-14 Sequence 14, Appli
C 7	413.4	27.5	816	4	US-09-352-616A-14 Sequence 14, Appli
C 8	413.4	27.5	816	4	US-09-232-149A-14 Sequence 14, Appli
C 9	413.4	27.5	816	4	US-09-159-812-14 Sequence 14, Appli
C 10	413.4	27.5	816	4	US-09-636-215-14 Sequence 14, Appli
C 11	413.4	27.5	816	4	US-09-685-166A-14 Sequence 14, Appli
C 12	413.4	27.5	816	4	US-09-115-453-14 Sequence 14, Appli
C 13	413.4	27.5	816	4	US-09-688-489-14 Sequence 14, Appli
C 14	357.8	23.8	760	3	US-09-020-956-37 Sequence 37, Appli
C 15	357.8	23.8	760	3	US-09-030-607-37 Sequence 37, Appli
C 16	357.8	23.8	760	4	US-09-439-313-37 Sequence 37, Appli
C 17	357.8	23.8	760	4	US-09-352-616A-37 Sequence 37, Appli
C 18	357.8	23.8	760	4	US-09-232-149A-37 Sequence 37, Appli
C 19	357.8	23.8	760	4	US-09-159-812-37 Sequence 37, Appli
C 20	357.8	23.8	760	4	US-09-636-215-37 Sequence 37, Appli
C 21	357.8	23.8	760	4	US-09-685-166A-37 Sequence 37, Appli
C 22	357.8	23.8	760	4	US-09-115-453-37 Sequence 37, Appli
C 23	357.8	23.8	760	4	US-09-688-489-37 Sequence 37, Appli
24	246.4	16.4	783	3	US-09-020-956-15 Sequence 15, Appli
25	246.4	16.4	783	3	US-09-030-607-15 Sequence 15, Appli
26	246.4	16.4	783	4	US-09-439-313-15 Sequence 15, Appli
27	246.4	16.4	783	4	US-09-352-616A-15 Sequence 15, Appli

28	246.4	16.4	783	4	US-09-232-149A-15 Sequence 15, Appli
29	246.4	16.4	783	4	US-09-159-812-15 Sequence 15, Appli
30	246.4	16.4	783	4	US-09-636-215-15 Sequence 15, Appli
31	246.4	16.4	783	4	US-09-685-166A-15 Sequence 15, Appli
32	246.4	16.4	783	4	US-09-115-453-15 Sequence 15, Appli
33	246.4	16.4	783	4	US-09-688-489-15 Sequence 15, Appli
34	177	11.8	399	4	US-09-312-283C-63 Sequence 63, Appli
35	174.4	11.6	399	3	US-09-188-930-63 Sequence 63, Appli
36	62.6	4.2	399	1	US-07-985-692-1 Sequence 1, Appli
37	62.6	4.2	399	1	US-08-155-331-1 Sequence 1, Appli
38	62.6	4.2	399	1	US-08-424-022-1 Sequence 1, Appli
39	62.6	4.2	399	2	US-08-424-017B-1 Sequence 1, Appli
40	62.6	4.2	399	5	PCT-US93-11696-1 Sequence 1, Appli
41	62.6	4.2	3725	1	US-08-155-331-12 Sequence 12, Appli
42	62.6	4.2	3725	1	US-08-424-022-12 Sequence 12, Appli
43	62.6	4.2	3725	2	US-08-424-017B-12 Sequence 12, Appli
44	62.6	4.2	3725	5	PCT-US93-11696-12 Sequence 12, Appli
45	53.8	3.6	344	1	US-07-972-387-9 Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-071-709-6
Sequence 6, Application US/09071709
Patent No. 6171790 - Chadda

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,709
FILING DATE: Filed Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0513 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1870 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOT04
CLONE: 1319265

US-09-071-709-6
Query Match 96.9%; Score 1458.6; DB 3; Length 1870;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTATGAGGCTGCTGGGCAACAAGAACAC 68
Db 398 CCCAOGGAGCAGATCTGCAAGAGTTTCGTTATGAGGCTGCTGGGCAACAAGAACAC 457
QY 69 TACCTTCGGGAGAGAGAGTGCAATCTAGCCTGTCGGGGTGTCAGAGTGGGCTTTGAGA 128
Db 458 TACCTTCGGGAGAGAGAGTGCAATCTAGCCTGTCGGGGTGTCAGAGTGGGCTTTGAGA 517
QY 129 GGCAGCTCTGGGCTCAGGCGACCTTCCCCAGGGCCCTCCATGGAAGGCGCCATCCA 188
Db 518 GGCAGCTCTGGGCTCAGGCGACCTTCCCCAGGGCCCTCCATGGAAGGCGCCATCCA 577
QY 189 GTGTCTCTGGCCTGTGAGCCACCCAGTTCCGCTGCAGCAATGCTGTCATGAC 248
Db 578 GTGTCTCTGGCCTGTGAGCCACCCAGTTCCGCTGCAGCAATGCTGTCATGAC 637
QY 249 AGTTTCCTGGAGTGTGACGACACCCCACTGCTCCGAGCGCTCCGAGGAGGCTGCTGT 308
Db 638 AGTTTCCTGGAGTGTGACGACACCCCACTGCTCCGAGCGCTCCGAGGAGGCTGCTGT 697
QY 309 GAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTCCCCAGCGACAAAGGG 368
Db 698 GAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTCCCCAGCGACAAAGGG 757
QY 369 CACTGCGTGGACCTGCCAGACACAGGACTCTCAAGGAGAGCATCCCGGCTGTACTAC 428
Db 758 CACTGCGTGGACCTGCCAGACACAGGACTCTCAAGGAGAGCATCCCGGCTGTACTAC 817
QY 429 AACCCCTTCAGCGAACACTGCGCCCGCTTTACTATGCTGTTTACGCAACAAGAAC 488
Db 818 AACCCCTTCAGCGAACACTGCGCCCGCTTTACTATGCTGTTTATGCAACAAGAAC 877
QY 489 AACTTTGAGGAAGAGCAGAGTGCCTCGAGTCTTGTGCGGCACTCTCAAGAGGATGTG 548
Db 878 AACTTTGAGGAAGAGCAGAGTGCCTCGAGTCTTGTGCGGCACTCTCAAGAGGATGTG 937
QY 549 TTTGGCCTGAGCGGGAATCCCATTCAGCAGAGGCTCTGTGGAGATGCTGTGCGCA 608
Db 938 TTTGGCCTGAGCGGGAATCCCATTCAGCAGAGGCTCTGTGGAGATGCTGTGCGCA 997
QY 609 GTGTTCTGCTCATCTGCAATGTTGTTGGTGTAGCATCTTGGTTACTGTTCTTCAAG 668
Db 998 GTGTTCTGCTCATCTGCAATGTTGTTGGTGTAGCATCTTGGTTACTGTTCTTCAAG 1057
QY 669 AACCAAGAGAAAGACTTCCAGCGACACCAACCCACCCACCCACCCCTGCCAGCTCC 728
Db 1058 AACCAAGAGAAAGACTTCCAGCGACACCAACCCACCCACCCACCCCTGCCAGCTCC 1117
QY 729 ACTGTCTCCACTACCGAGGACACGAGCCTGCTGTATTAACCAACCAACCGGCGCCCTC 788
Db 1118 ACTGTCTCCACTACCGAGGACACGAGCCTGCTGTATTAACCAACCAACCGGCGCCCTC 1177
QY 789 TGAGCCTGGGTCTCACCGGCTCTCACCTGCGCCCTGCTTCTGCTTGCCTGAGGAGGCC 848
Db 1178 TGAGCCTGGGTCTCACCGGCTCTCACCTGCGCCCTGCTTCTGCTTGCCTGAGGAGGCC 1237
QY 849 TGGGCTGGGAAAGAACTTTGGAACCAAGACTCTTGCTGTTTCCAGGCGCCACTGCTCA 908
Db 1238 TGGGCTGGGAAAGAACTTTGGAACCAAGACTCTTGCTGTTTCCAGGCGCCACTGCTCA 1297
QY 909 GAGACAGGGCTCCAGCCCTCTTGGAGAGTCTCAGTAAAGTCTCAGTCTCTGAGAAAGC 968
Db 1298 GAGACAGGGCTCCAGCCCTCTTGGAGAGTCTCAGTAAAGTCTCAGTCTCTGAGAAAGC 1357
QY 969 TCAAAGTTTGAAGGAGCAGAAACCTTGGGCCAGAGTACCAAGACTAGATGAGCCTG 1028
Db 1358 TCAAAGTTTGAAGGAGCAGAAACCTTGGGCCAGAGTACCAAGACTAGATGAGCCTG 1417
QY 1029 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTTCAAAGCTGCTTCC 1088
Db 1418 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTGTTCCTCTGTTCAAAGCTGCTTCC 1477

QY 1089 CTACCCCATGGTCTAGGAAGAGGAGTGGGTGTTGTTGAGACCTTGAGGCCCCAACCCCT 1148
Db 1478 CTACCCCATGGTCTAGGAAGAGGAGTGGGTGTTGTTGAGACCTTGAGGCCCCAACCCCT 1537
QY 1149 GTCTCCCGAGCTCCTCTTCCATGCTGTGCGCCAGGCTGGGAGGAAGGACTTCCCTGT 1208
Db 1538 GTCTCCCGAGCTCCTCTTCCATGCTGTGCGCCAGGCTGGGAGGAAGGACTTCCCTGT 1597
QY 1209 GTAGTTTGTGCTGTAAGAGTGTCTTTTGTATTATTAAATGCTGTGGCATGGGTGAAGAG 1268
Db 1598 GTAGTTTGTGCTGTAAGAGTGTCTTTTGTATTATTAAATGCTGTGGCATGGGTGAAGAG 1657
QY 1269 GAGGGAAGAGGCTCTTGTGCTCTCTATCCTCTCTTCTCTTCCCAAGATTGAGCT 1328
Db 1658 GAGGGAAGAGGCTCTTGTGCTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1717
QY 1329 CTCTGCCCTTGATCAGCCCGCCCTGGCCTAGACCAGACAGAGCCAGGAGAGCTCA 1388
Db 1718 CTCTGCCCTTGATCAGCCCGCCCTGGCCTAGACCAGACAGAGCCAGGAGAGCTCA 1777
QY 1389 GCTGCATTCCGAGCCCGCCCTCCCAAGGTTCTCCAAATCAGACCCAGCCCGCCACT 1448
Db 1778 GCTGCATTCCGAGCCCGCCCTCCCAAGGTTCTCCAAATCAGACCCAGCCCGCCACT 1837
QY 1449 GGGTAATAAAGTGGTTTGTGGAAAAA 1481
Db 1838 GGGTAATAAAGTGGTTTGTGGAAAAA 1870

RESULT 2

US-08-685-558A-8
; Sequence 8, Application US/08685558A
; Patent No. 6225081
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; APPLICANT: MIYAZAWA, Keiji
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,558A
; FILING DATE: 24-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JPA Hei 7-187135
; FILING DATE: 24-JUL-1995
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: MKN45
; FEATURE:
; NAME/KEY: coding sequence
; LOCATION: 1 to 1542

IDENTIFICATION METHOD: by experiment
NAME/KEY: signal peptide
LOCATION: 1 to 105
IDENTIFICATION METHOD: by experiment
NAME/KEY: mature peptide
LOCATION: 106 to 1542
IDENTIFICATION METHOD: by experiment
US-08-685-558A-8

Query Match 44.3%; Score 667.4; DB 3; Length 1542;
Best Local Similarity 93.1%; Pred. No. 3.3e-168;
Matches 729; Conservative 0; Mismatches 6; Indels 48; Gaps 1;

QY 9 CACGAGGACGAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTGGGCAACAAGAACAC 68
DB 808 CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTGGGCAACAAGAACAC 867
QY 69 TACCTTCGGGAAGAAGAGTGCAATCTAGCCTGTGCGGGTGTGCAAGGTGGCCCTTTGAGA 128
DB 868 TACCTTCGGGAAGAAGAGTGCAATCTAGCCTGTGCGGGTGTGCAAGGTGGCCCTTTGAGA 912
QY 129 GGCAGCTCTGGGGCTCAGGCGACTTTCGCCAGGGCCCTCCATGGAAGGCGCCATCCA 188
DB 913 -----GGCCCCCTCCATGGAAGGCGCCATCCA 939
QY 189 GTGTGCTCTGGCACCCTGTGAGCCACCCAGTTCCGCTGAGCAATGGCTGCTGCATCGAC 248
DB 940 GTGTGCTCTGGCACCCTGTGAGCCACCCAGTTCCGCTGAGCAATGGCTGCTGCATCGAC 999
QY 249 AGTTTCTCTGGAGTGTGACGACACCCCACTGCCCGAGCGCTCCGACGAGGCTGCCTGT 308
DB 1000 AGTTTCTCTGGAGTGTGACGACACCCCACTGCCCGAGCGCTCCGACGAGGCTGCCTGT 1059
QY 309 GAAATAATACAGAGTGGCTTTCAGGAGCTCCAGGCGCATCCATTTCCCGAGCGCAAGGG 368
DB 1060 GAAATAATACAGAGTGGCTTTCAGGAGCTCCAGGCGCATCCATTTCCCGAGCGCAAGGG 1119
QY 369 CACTGCGTGGACCTGCGCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCTGGTACTAC 428
DB 1120 CACTGCGTGGACCTGCGCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCTGGTACTAC 1179
QY 429 AACCCCTTCAGCGAACAACCTGGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAAC 488
DB 1180 AACCCCTTCAGCGAACAACCTGGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAAC 1239
QY 489 AACTTTGAGGAAGAGCAGTGCCTCGAGTCTGTGCGGGCATCTCCAAAGAGGATGTG 548
DB 1240 AACTTTGAGGAAGAGCAGTGCCTCGAGTCTGTGCGGGCATCTCCAAAGAGGATGTG 1299
QY 549 TTTGGCCTGAGGCGGGAATCCCATTCACGACAGGCTCTGTGAGATGGCTGTGCGCA 608
DB 1300 TTTGGCCTGAGGCGGGAATCCCATTCACGACAGGCTCTGTGAGATGGCTGTGCGCA 1359
QY 609 GTGTTCTCTGGTCAATCTGCAATGTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 668
DB 1360 GTGTTCTCTGGTCAATCTGCAATGTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 1419
QY 669 AACGAGAGAAAGGACTTCCACGGACACCCACCCACCCACCCCTGCGCAGCTCC 728
DB 1420 AACGAGAGAAAGGACTTCCACGGACACCCACCCACCCACCCCTGCGCAGCTCC 1479
QY 729 ACTGTCTCCACTACCGAGGACACGGAGCACTGGTGTATAACCCACACACCGGCGCCCTC 788
DB 1480 ACTGTCTCCACTACCGAGGACACGGAGCACTGGTGTATAACCCACACACCGGCGCCCTC 1539
QY 789 TGA 791
DB 1540 TGA 1542

RESULT 3

US-09-765-449-8

; Sequence 8, Application US/09765449

Patent No. 6465622
GENERAL INFORMATION:
APPLICANT: SHIMOMURA, Takeshi
KAWAGUCHI, Toshiya
KITAMURA, Naomi
MIYAZAWA, Keiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
AND METHOD OF PRODUCING THE PROTEIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,449
FILING DATE: 22-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,558
FILING DATE: <Unknown>
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 1542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: MKN45
FEATURES:
SEQUENCE DESCRIPTION: SEQ ID NO: 8
US-09-765-449-8

Query Match 44.3%; Score 667.4; DB 4; Length 1542;
Best Local Similarity 93.1%; Pred. No. 3.3e-168;
Matches 729; Conservative 0; Mismatches 6; Indels 48; Gaps 1;

QY 9 CACGAGGACGAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTGGGCAACAAGAACAC 68
DB 808 CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTGGGCAACAAGAACAC 867
QY 69 TACCTTCGGGAAGAAGAGTGCAATCTAGCCTGTGCGGGTGTGCAAGGTGGCCCTTTGAGA 128
DB 868 TACCTTCGGGAAGAAGAGTGCAATCTAGCCTGTGCGGGTGTGCAAGGTGGCCCTTTGAGA 912
QY 129 GGCAGCTCTGGGGCTCAGGCGACTTTCGCCAGGGCCCTCCATGGAAGGCGCCATCCA 188
DB 913 -----GGCCCCCTCCATGGAAGGCGCCATCCA 939
QY 189 GTGTGCTCTGGCACCCTGTGAGCCACCCAGTTCCGCTGAGCAATGGCTGCTGCATCGAC 248
DB 940 GTGTGCTCTGGCACCCTGTGAGCCACCCAGTTCCGCTGAGCAATGGCTGCTGCATCGAC 999
QY 249 AGTTTCTCTGGAGTGTGACGACACCCCACTGCCCGAGCGCTCCGACGAGGCTGCCTGT 308
DB 1000 AGTTTCTCTGGAGTGTGACGACACCCCACTGCCCGAGCGCTCCGACGAGGCTGCCTGT 1059
QY 309 GAAATAATACAGAGTGGCTTTCAGGAGCTCCAGGCGCATCCATTTCCCGAGCGCAAGGG 368
DB 1060 GAAATAATACAGAGTGGCTTTCAGGAGCTCCAGGCGCATCCATTTCCCGAGCGCAAGGG 1119
QY 369 CACTGCGTGGACCTGCGCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCTGGTACTAC 428
DB 1120 CACTGCGTGGACCTGCGCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCTGGTACTAC 1179

QY 429 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTTACGCGAACCAAGAAC 488
Db 1180 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTTATGCGAACCAAGAAC 1239
QY 489 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTGTGCGGCATCTCCAGAAAGGATGTG 548
Db 1240 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTGTGCGGCATCTCCAGAAAGGATGTG 1299
QY 549 TTTGGCCTGAGGCGGGAATCCCATTTCCAGCAGGCTCTGTGGAGATGGCTGTGCGCA 608
Db 1300 TTTGGCCTGAGGCGGGAATCCCATTTCCAGCAGGCTCTGTGGAGATGGCTGTGCGCA 1359
QY 609 GTGTTCTCTGTCATCTGCATTTGTTGGTGGTAGCCATCTTGGGTTACTGTTCTTCAAG 668
Db 1360 GTGTTCTCTGTCATCTGCATTTGTTGGTGGTAGCCATCTTGGGTTACTGTTCTTCAAG 1419
QY 669 AACAGAGAAAGGACTTCCAGCGACACCCACCCACCCACCCCTGCCAGCTCC 728
Db 1420 AACAGAGAAAGGACTTCCAGCGACACCCACCCACCCACCCCTGCCAGCTCC 1479
QY 729 ACTGTCTCCACTACCGAGGACAGGAGCAGGACCTGTCTATACCCACCCACCCGCGCCCTC 788
Db 1480 ACTGTCTCCACTACCGAGGACAGGAGCAGGACCTGTCTATACCCACCCACCCGCGCCCTC 1539
QY 789 TGA 791
Db 1540 TGA 1542

RESULT 4
US-09-020-956-14/c
; Sequence 14, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-020-956-14

Query Match 27.5%; Score 413.4; DB 3; Length 816;
Best Local Similarity 92.0%; Pred. No. 1.3e-100;

Matches 459; Conservative 0; Mismatches 37; Indels 3; Gaps 3;
QY 9 CACGAGAGCAGATCTGCAAGAGTTTCTGTTTATGGAGGCTGCTTGGGCAACAAGAAC 68
Db 498 CCGCAGAGCAGATNTGCAAGAGTTT-GTTTANGGGGNTGGTGGGCAACAAGAAC 440
QY 69 TACC-TTCGGGAAGAAGAGTGCATTCTAGCCTGTGCGGGTGTGCAAGGT-GGGCCTTTGA 126
Db 439 TACCTTTCCGGGAAGAAGATTCCATTCTAGCCTGTGCGGGTGTGCAAGGTGGGCTTTGA 380
QY 127 GAGGAGCTCTGGGGCTCAGGCGACTTTCCCCAGGGCCCCCTCCATGGAAAGCGCCATC 186
Db 379 GAGGAGCTNTGGGGTTCAGGAGACTTTCCNCAGGGCCCCCTCCATGGAAAGCGCCATC 320
QY 187 CAGTGTCTCTGGCACCTGTGAGCCACCCAGTTCGGCTGCGAATGCTGCTGCTGCTG 246
Db 319 CAGTGTCTCTGGCACNTGTGAGCCACCCAGTTCGGCTGCGAATGCTGCTGCTGCTG 250
QY 247 ACAGTTTCTGAGTGTGACGACACCCCAACTGCCCGAGCGCTCCGACGAGGCTGCCT 306
Db 259 ACAGTTTCTGAGTGTGAGAGACACCCCAACTGCCCGAGCGCTCCGACGAGGCTGCCT 200
QY 307 GTGAAATAACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCGACAAG 366
Db 199 GTGAAATAACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGTGACAAG 140
QY 367 GGCAGTGGTGGACCTGCCAGACAGGACTCTGCAAGGAGAGCATCCCGCGCTGTACT 426
Db 139 GGCAGTGGTGGACCTGCCAGACAGGACTCTGCAAGGAGAGCATCCCGCGCTGTACT 80
QY 427 ACAACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTGTGTTACGGAACAAGA 486
Db 79 ACAACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTGTGTTATGGCAACAAGA 20
QY 487 ACAACTTTGAGGAAGAGCA 505
Db 19 ACAACTTTGAGGAAGAGCA 1

RESULT 5
US-09-030-607-14/c
; Sequence 14, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS F
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:


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; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-030-607-14

Query Match      27.5%; Score 413.4; DB 3; Length 816;
Best Local Similarity 92.0%; Pred. No. 1.3e-100;
Matches 459; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

QY 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGCAAC 68
Db 498 CCCNCGGAGCAGATNTGCAAGAGTTT-GTTTANGGGGNTGNTTGGGCAACAAGANAAC 440

QY 69 TACC-TTCGGGAAGAAGAGTGCAATCTAGCCTGTGCGGGTGTGCAAGGT-GGGCCTTTGA 126
Db 439 TACCTTTTCGGGAAGAAGATTCCATTTCTAGCCTGTGCGGGTGTGCAAGGTGGGCGCTTTGA 380

QY 127 GAGGCAGCTCTGGGCTCAGGCGACTTTTCCCCAGGGGCCCTCCATGGAAGGGCGCCATC 186
Db 379 GAGGCAGNTNTGGGNTCAGGGAATTTCCCNAGGGGCCNTNNCATGGAAGGGCGCCATC 320

QY 187 CAGTGTGCTCTGGCACCTGTGAGCCCAACCCAGTTCGCTGCAGCAATGGCTGCTGCATCG 246
Db 319 CAGTGTGCTCTGGCACNTGTGAGCCCAACCCAGTTCGCTGCAGCAATGGCTGCTGCATNG 260

QY 247 ACAGTTTCTGGAGTGTGACGACACCCCACTGCGCCCGACCGCTCCGACGAGGCTGCCT 306
Db 259 ACAGTTTCTGGAGTGTGAGACACCCCACTGCGCCCGACCGCTCCGACGAGGCTGCCT 200

QY 307 GTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGACGCAAAAG 366
Db 199 GTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGACGCAAAAG 140

QY 367 GGCACCTGGTGAACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGTGGTACT 426
Db 139 GGCACCTGGTGAACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGTGGTACT 80

QY 427 ACAACCCCTTCAGCGAACACTGCGCCCGCTTACCTATGTTGTTTACGGCAACAAGA 486
Db 79 ACAACCCCTTCAGCGAACACTGCGCCCGCTTACCTATGTTGTTTATGGCAACAAGA 20

QY 487 ACAACTTTGAGGAAGAGCA 505
Db 19 ACAACTTTGAGGAAGAGCA 1
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RESULT 6
US-09-439-313-14/c
; Sequence 14, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(816)
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; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-14

Query Match      27.5%; Score 413.4; DB 4; Length 816;
Best Local Similarity 92.0%; Pred. No. 1.3e-100;
Matches 459; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

QY 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGCAAC 68
Db 498 CCCNCGGAGCAGATNTGCAAGAGTTT-GTTTANGGGGNTGNTTGGGCAACAAGANAAC 440

QY 69 TACC-TTCGGGAAGAAGAGTGCAATCTAGCCTGTGCGGGTGTGCAAGGT-GGGCCTTTGA 126
Db 439 TACCTTTTCGGGAAGAAGATTCCATTTCTAGCCTGTGCGGGTGTGCAAGGTGGGCGCTTTGA 380

QY 127 GAGGCAGCTCTGGGCTCAGGCGACTTTTCCCCAGGGGCCCTCCATGGAAGGGCGCCATC 186
Db 379 GAGGCAGNTNTGGGNTCAGGGAATTTCCCNAGGGGCCNTNNCATGGAAGGGCGCCATC 320

QY 187 CAGTGTGCTCTGGCACCTGTGAGCCCAACCCAGTTCGCTGCAGCAATGGCTGCTGCATCG 246
Db 319 CAGTGTGCTCTGGCACNTGTGAGCCCAACCCAGTTCGCTGCAGCAATGGCTGCTGCATNG 260

QY 247 ACAGTTTCTGGAGTGTGACGACACCCCACTGCGCCCGACCGCTCCGACGAGGCTGCCT 306
Db 259 ACAGTTTCTGGAGTGTGAGACACCCCACTGCGCCCGACCGCTCCGACGAGGCTGCCT 200

QY 307 GTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGACGCAAAAG 366
Db 199 GTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCGACGCAAAAG 140

QY 367 GGCACCTGGTGAACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGTGGTACT 426
Db 139 GGCACCTGGTGAACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGTGGTACT 80

QY 427 ACAACCCCTTCAGCGAACACTGCGCCCGCTTACCTATGTTGTTTACGGCAACAAGA 486
Db 79 ACAACCCCTTCAGCGAACACTGCGCCCGCTTACCTATGTTGTTTATGGCAACAAGA 20

QY 487 ACAACTTTGAGGAAGAGCA 505
Db 19 ACAACTTTGAGGAAGAGCA 1
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RESULT 7
US-09-352-616A-14/c
; Sequence 14, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427CB
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(816)
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; OTHER INFORMATION; n = A, T, C or G
US-09-352-616A-14

Query Match	27.5%	Score 413.4;	DB 4;	Length 816;
Best Local Similarity	92.0%;	Pred. No. 1.3e-100;		
Matches 459;	Conservative	0;	Mismatches 37;	Indels 3;
				Gaps 3;

QY		9	CACGAGGAGCAGATCTGCAAGAGTTTCGTATTAGGAGGCTGCTGGGCCAACAGACAAC	68
Dd		498	CCCNCGGAGCAGTNTGCAAGAGTTT-GTTTTANGGGNTGNTTGGCCAACAAGANAAC	440
QY		69	TACC-TTCGGGAAGAAGAGTGCAATTCATAGCCTGTGCGGGGTGTGCAAGGT- GGGCCCTTGA	126
Dd		439	TACCTTTTCGGGAAGAAGATTCATTTCTAGCCTGTGCGGGGTGTGCAAGGTGGGGCNTTTGA	380
QY		127	GAGGCAGCTCTGGGGCTCAGGCGACTTTCCCCCAGGGGCCCTCCATGGAAAGGGGCCATC	186
Dd		379	GAGGCAGNNTGSGGNTCAGGGACTTTCCNCAGGGCCNTNNCATGGAAAGGGGCCATC	320
QY		187	CAGTGTCTCTGGCACCTGTTCAGCCCACCCAGTTCGGTGCAGCAATGGCTGTGCATCG	246
Dd		319	CAGTGTCTCTGGCAGTGTTCAGCCCACCCAGTTCGGTGCAGCAATGGCTGTGCATNG	260
QY		247	ACAGTTTCCTGGAGTGTGACGACACCCCCCAACTGCCCGCAGCGCTCCGACGAGGCTGCCT	306
Dd		259	ACAGTTTCCTGGAGTGTGAAGACACCCCCCAACTGCCCGCAGCGCTCGGACGAGGCTGCCT	200
QY		307	GTGAAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCACGCGACAAG	366
Dd		199	GTGAAAATAACAGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCAGTGACAAG	140
QY		367	GGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACT	426
Dd		139	GGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACT	80
QY		427	ACAACCCCTTCAGCGAACA CTGGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAGA	486
Dd		79	ACAACCCCTTCAGCGAACA CTGGCCCGCTTTACCTATGGTGGTTGTTATGGCAACAAGA	20
QY		487	ACRACTTTGAGGAAGGCA	505
Dd		19	ACRACTTTGAGGAAGGCA	1

RESULT 8

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RES011 8
US-09-232-149A-14/c
; Sequence 14, Application US/09232149A
; Patent No. 6465612
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14

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LENGTH: 816
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(816)
OTHER INFORMATION: n = A,T,C or G
S-09-232-149A-14

Query Match          27.5%;      Score 413.4;   DB 4;      Length 816;
Best Local Similarity 92.0%;      Pred. No. 1.3e-100;
Matches 459; Conservative 0; Mismatches 37; Indels 3; Gaps 3

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QY	9	CACGAGGACGACATCTGCAAGAGCTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAAC	68
DB	498	CCNCGGAGCAGATNTGCAAGAGTTT-CTTTANGGGGENTGGNTTGGGCAACAAGANAAC	440
QY	69	TACC-TTCGGGAAGAAGAGTGCAATTCCTACCTGTTCGGGGTGTGCAAGGT--GGGCTTTTGA	126
DB	439	TACCTTTTCGGGAAGAAGATTCCATTTCTAGCTGTTCGGGGTGTGCAAGGTTCGGGCTTTGA	380
QY	127	GAGGCAGCTCTGGGGCTCAGGGGACTTTCCTCCACAGGGCCCCCTCCATGGAAAGGCGCCATC	186
DB	379	GAGGCAGTNTGGGNTCAGGGACTTTCCTCCNCAAGGGCCCCNTNNNCATGGAAAGGCGCCATC	320
QY	187	CAGTGTGCTCTGGCACCTGTGCAGCCCCACCCAGTTCCGCTGCAGCAATGGCTGTGTCATCG	246
DB	319	CAGTGTGCTCTGGCANTGTGCAGCCCCACCCAGTTCCGCTGCAGCAATGGCTGTGTCATNG	260
QY	247	ACAGTTTCTCGAGTGTGACGACACCCCCCAACTGCCCCGACCGCTTCGACGAGGCTGCCT	306
DB	259	ACAGTTTCTCGAGTGTGAAGACACCCCCCAACTGCCCCGACCGCTTCGACGAGGCTGCCT	200
QY	307	GTGAAAAATACACGAGTGGCTTTGACGAGTCTCCAGCGCATCCATTTCCCGACGCAACAAG	366
DB	199	GTGAAAAATACACGAGTGGCTTTGACGAGTCTCCAGCGCATCCATTTCCCGACGCAACAAG	140
QY	367	GGCAGTCGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACT	426
DB	139	GGCAGTCGCTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACT	80
QY	427	ACAACCCCTTTCAGCGAAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGA	486
DB	79	ACAACCCCTTTCAGCGAAACACTGCGCCCGCTTTACCTATGGTGGTTGTTATGGCAACAAGA	20
QY	487	ACAACCTTTGAGGAAGAGCA	505
DB	19	ACAACCTTTGAGGAAGAGCA	1

RESIT, T 9

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US-09-159-812-14/c
; Sequence 14, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A,T,C or G
;
US-09-159-812-14

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Query Match	27.5%;	Score 413.4;	DB 4;	Length 816;
Best Local Similarity	92.0%;	Pred. No. 1.3e-100;		
Matches 459.	Conservative	0;	Mismatches 37;	Indels 3;
				Gaps 3;

QY		9	CACGAGGAGCAGATCGCAAGAGTTTCGTTTATGGAGCCTGTGGGCAACAAGAAC	68
Dδ		498	CCNCGGAGCAGATTGCAAGAGTTT-GTTTANGGGGTGNTTGGGCAACAAGANAAC	440
QY		69	TACC-TTCGGGAAGAAGTGCATTTAGCCCTGTGGGTGTGCAAGGT-GGGCCTTTGA	126
Dδ		439	TACCTTTTCGGGAAGAAGATTCATTTAGCCCTGTGGGGTGTGCAAGGTGGGCNITTGA	380

Db 379 GAGGAGNTGGGNTCAGGGACTTCCNCAGGGCCCTNNCATGGAAGGGCGCATC 320
QY 187 CAGTGTCTCTGGCACCTGTGAGCCACCCAGTTCCGCTGCAGCAATGGCTGCTGCATCG 246
Db 319 CAGTGTCTCTGGCACNTGTGAGCCACCCAGTTCCGCTGCAGCAATGGCTGCTGCATNG 260
QY 247 ACAGTTTCTGGAGTGTGACGACACCCCAACTGCCCGAGCGCTCCGACGAGGCTGCCT 306
Db 259 ACAGTTTCTGGAGTGTGAGACACCCCAACTGCCCGAGCGCTCCGACGAGGCTGCCT 200
QY 307 GTGAAAAATACACGAGTGGCTTTGAGGAGCTCCAGCGCATCCATTTCCCGAGCGACAAAG 366
Db 199 GTGAAAAATACACGAGTGGCTTTGAGGAGCTCCAGCGCATCCATTTCCCGAGTACAAAG 140
QY 367 GGCAGTGGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCTGGTACT 426
Db 139 GGCAGTGGTGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGGCTGGTACT 80
QY 427 ACAACCCCTTCAGCGAACACTGGCGCCGCTTACCTATGGTGTGTTACGGCAACAGA 486
Db 79 ACAACCCCTTCAGCGAACACTGGCGCCGCTTACCTATGGTGTGTTATGGCAACAGA 20
QY 487 ACAACTTTCAGGAAGAGCA 505
Db 19 ACAACTTTCAGGAAGAGCA 1

RESULT 14
US-09-020-956-37/c
; Sequence 37, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 760 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-020-956-37

Query Match 23.8%; Score 357.8; DB 3; Length 760;
Best Local Similarity 90.2%; Pred. No. 8.4e-86;
Matches 432; Conservative 0; Mismatches 39; Indels 8; Gaps 5;

QY 32 TTTCGTTTATGAGGCTGCTGGGCAACAAGAACTACCTTCGGGAAGAGAGTGCA- 90
Db 476 TTGCTTTGNTGGAGNTGCTTGGGCAACAAGAACTACCTTTGGGAAGAGAGTGCA 417
QY 91 TTCTAGCCTGTCGGGCTGTGCAAGTGGGCTTTGAGAGGCGAGCTCTGGGGCTCAGCGA 150
Db 416 TTCTAGCCTGTCGGGCTGTGCAAGT-GGCTTTTGGAGGCGAGTTTGGG-----NTNAGGN 362
QY 151 CTTTCCCCCAGGGCCCTCCATGGAAGGGCGCCATCCAGTGTCTCTGGCACCTGTCAGC 210
Db 361 GATTTCCCCCAGGGCCCTCCATGGAAGGC-CNATCCAGTGTGTTCTGGCACCTGTCAGC 303
QY 211 CCACCCAGTTCGGCTGCAGCAAT-GGCTGCTGCATCGACAGTTTCTCTGGAGTGTGACGAC 269
Db 302 CCACCCAGTTCGGCTGCAGCAATGGGCTGNTGATCGACAGTTTAGTGGAGTGTGACGAC 243
QY 270 ACCCCCAACTGCCCCGAGCGCTCCGACGAGGCTGCTGTAATAATACAGAGTGGCTTT 329
Db 242 ACCCCCAACTGCCCCGAGCGCTTCGGAGGAGGCTGCTGTAATAATACAGAGTGGNTTN 183
QY 330 GACGAGCTCCAGCGCATCTTCCCGAGCGCAAGAGGCACTGCTGGGACCTGCCAGAC 389
Db 182 GACGAGCTCCAGCGCATCTTCCCGAGCGCAAGAGGCACTGCTGGGACCTGCCAGAC 123
QY 390 ACAGGACTCTGCAAGGAGAGGAGCATCCCGGCTGTTACTACAACTTCAGCGAAGAGTGC 449
Db 122 ACAGGACTCTGCAAGGAGAGGAGCATCCCGGCTGTTACTACAACTTCAGCGAAGAGTGC 63
QY 450 GCGCGCTTTACTATGTTGTTGTTTACGGCAACAAGAACTTTTGAGGAAGAGAGCA 508
Db 62 GCGCGCTTTACTATGTTGTTGTTTATGGCAACAAGAACTTTTGAGGAAGAGAGCA 4

RESULT 15
US-09-030-607-37/c
; Sequence 37, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FC
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 760 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-030-607-37

Query Match		23.8%;	Score 357.8;	DB 3;	Length 760;
Best Local Similarity		90.2%;	Pred. NO. 8.4e-86;		
Matches 432;		Conservative 0;	Mismatches 39;	Indels 8;	Gaps 5;
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Db	476	TTGGTTTGNNTGGAGGNTGCTTGGGCAACAAGAACAACTACCTTTGGGAAGAGAGTGCA	417		
Qy	91	TTCTAGCCTGTCCGGGGTGTGCAAGGTGGGCCCTTTGAGAGGCAGCTCTGGGGCTCAGGCCA	150		
Db	416	TTCTAGCCTGTCCGGGGTGTGCAAGGT-GGCCCTTGAGAGGCAGTTTGGG-----NTNAGGN	362		
Qy	151	CTTTCCCCCAGGGCCCCCTCCATGGAAGGGGCCATCCAGTGTCTCTGGCACTGTTCAGC	210		
Db	361	GATTTCCCCCAGGGCCCCCTCCATGGAAGGC-CNATCCAGTGTGTTCTGGCACTGTTCAGC	303		
Qy	211	CCACCCAGTTCGGCTGCAGCAAT-GGCTGCTGCATCGACAGTTTCCTGGAGTGTGACGAC	269		
Db	302	CCACCCAGTTCGGCTGCAGCAATGGGCTGNTGNATCGACAGTTTGTGGAGTGTGACGAC	243		
Qy	270	ACCCCAACTGCCCGGACGCTCCGACGAGGCTGCCTGTGAAAAATACACAGTGGCTTT	329		
Db	242	ACCCCAACTGCCCGGANGCTTCGGAGGAGGCTGCNTGTGAAAAATACACAGTGGNTTN	183		
Qy	330	GACGAGCTCCAGCGCATCCATTTCCCAGCGACAAAGGGCACTGCGTGGACCTGCCAGAC	389		
Db	182	GACGAGCTCCAGCGCATCCATTTCCCAGTGCACAAAGGGCACTGCGTGGACCTGCCAGAC	123		
Qy	390	ACAGGACTCTGCAAGGAGAGCATCCCGCGTGGTACTACAACCCCTTCAGCGAACACTGC	449		
Db	122	ACAGGACTCTGCAAGGAGAGCATCCCGCGTGGTACTACAACCCCTTCAGCGAACACTGC	63		
Qy	450	GCCCGCTTTACCTATGGTGTGTTTACGGCAACAAGAACAACTTTGAGGAAGAGCAGCA	508		
Db	62	GCCCGCTTTACCTATGGTGTGTTTATGGCAACAAGAACAACTTTGAGGAAGAGCAGCA	4		

Search completed: April 22, 2004, 08:12:04
Job time : 125 secs

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OM protein - protein search, using sw model

Run on: April 22, 2004, 10:22:35 ; Search time 23 Seconds
(without alignments)
462.369 Million cell updates/sec

Title: US-09-935-390A-23
Perfect score: 206
Sequence: 1 MERRHPVCSGTCQPTQFRCS.....TVSTTEDTEHLVYNHTTTP 206

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	206	100.0	348	3 US-09-071-709-2	Sequence 2, Appli
2	206	100.0	513	3 US-08-685-558A-18	Sequence 18, Appl
3	206	100.0	513	4 US-09-765-449-18	Sequence 18, Appl
4	27	13.1	72	4 US-09-312-283C-182	Sequence 182, App
5	21	10.2	72	3 US-09-188-930-182	Sequence 182, App
6	11	5.3	38	6 5208144-20	Patent No. 5208144
7	11	5.3	726	6 5208144-37	Patent No. 5208144
8	8	3.9	1241	3 US-09-040-774-2	Sequence 2, Appli
9	7	3.4	58	1 US-08-566-800A-32	Sequence 32, Appl
10	7	3.4	58	1 US-08-566-800A-37	Sequence 37, Appl
11	7	3.4	58	1 US-08-566-800A-38	Sequence 38, Appl
12	7	3.4	58	1 US-08-566-800A-39	Sequence 39, Appl
13	7	3.4	58	1 US-08-566-800A-42	Sequence 42, Appl
14	7	3.4	58	1 US-08-566-800A-44	Sequence 44, Appl
15	7	3.4	58	1 US-08-566-800A-45	Sequence 45, Appl
16	7	3.4	58	1 US-08-566-800A-47	Sequence 47, Appl
17	7	3.4	58	1 US-08-566-800A-51	Sequence 51, Appl
18	7	3.4	58	1 US-08-566-800A-52	Sequence 52, Appl
19	7	3.4	58	1 US-08-566-800A-53	Sequence 53, Appl
20	7	3.4	58	1 US-08-566-800A-54	Sequence 54, Appl
21	7	3.4	58	1 US-08-566-800A-57	Sequence 57, Appl
22	7	3.4	58	1 US-08-206-310A-33	Sequence 33, Appl
23	7	3.4	58	2 US-08-398-010A-33	Sequence 33, Appl
24	7	3.4	58	2 US-08-398-010A-47	Sequence 47, Appl
25	7	3.4	58	2 US-08-398-010A-52	Sequence 52, Appl
26	7	3.4	58	2 US-08-398-010A-53	Sequence 53, Appl
27	7	3.4	58	2 US-08-398-010A-54	Sequence 54, Appl

28	7	3.4	58	2 US-08-398-010A-57	Sequence 57, Appl
29	7	3.4	58	2 US-08-398-010A-59	Sequence 59, Appl
30	7	3.4	58	2 US-08-398-010A-60	Sequence 60, Appl
31	7	3.4	58	2 US-08-398-010A-62	Sequence 62, Appl
32	7	3.4	58	2 US-08-398-010A-66	Sequence 66, Appl
33	7	3.4	58	2 US-08-398-010A-67	Sequence 67, Appl
34	7	3.4	58	2 US-08-398-010A-68	Sequence 68, Appl
35	7	3.4	58	2 US-08-398-010A-69	Sequence 69, Appl
36	7	3.4	58	2 US-08-398-010A-72	Sequence 72, Appl
37	7	3.4	58	2 US-08-398-628A-33	Sequence 33, Appl
38	7	3.4	58	2 US-08-398-628A-47	Sequence 47, Appl
39	7	3.4	58	2 US-08-398-628A-52	Sequence 52, Appl
40	7	3.4	58	2 US-08-398-628A-53	Sequence 53, Appl
41	7	3.4	58	2 US-08-398-628A-54	Sequence 54, Appl
42	7	3.4	58	2 US-08-398-628A-57	Sequence 57, Appl
43	7	3.4	58	2 US-08-398-628A-59	Sequence 59, Appl
44	7	3.4	58	2 US-08-398-628A-60	Sequence 60, Appl
45	7	3.4	58	2 US-08-398-628A-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-09-071-709-2
; Sequence 2, Application US/09071709
; Patent No. 6171790
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,709
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0513 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT04
; CLONE: 1319265
US-09-071-709-2

Query Match 100.0%; Score 206; DB 3; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.1e-187;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
Db 143 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 202
Qy 61 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCFRTYGGCYGNKNFEEQQCLESCRG 120
Db 203 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCFRTYGGCYGNKNFEEQQCLESCRG 262
Qy 121 ISKDVFGRLRREIPSTGSEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 180
Db 263 ISKDVFGRLRREIPSTGSEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 322
Qy 181 PTPASSTVSTTEDTEHLVYNHTTRPL 206
Db 323 PTPASSTVSTTEDTEHLVYNHTTRPL 348

RESULT 2
US-08-685-558A-18
Sequence 18, Application US/08685558A
Patent No. 6225081
GENERAL INFORMATION:
APPLICANT: SHIMOMURA, Takeshi
APPLICANT: KAWAGUCHI, Toshiya
APPLICANT: KITAMURA, Naomi
APPLICANT: MIYAZAWA, Keiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,558A
FILING DATE: 24-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPA Hei 7-187135
FILING DATE: 24-JUL-1995
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: MKN45

Query Match 100.0%; Score 206; DB 3; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
Db 308 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 367
Qy 61 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCFRTYGGCYGNKNFEEQQCLESCRG 120
Db 368 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCFRTYGGCYGNKNFEEQQCLESCRG 427
Qy 121 ISKDVFGRLRREIPSTGSEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 180

Db 428 ISKDVFGRLRREIPSTGSEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 487
Qy 181 PTPASSTVSTTEDTEHLVYNHTTRPL 206
Db 488 PTPASSTVSTTEDTEHLVYNHTTRPL 513
RESULT 3
US-09-765-449-18
Sequence 18, Application US/09765449
Patent No. 6465622
GENERAL INFORMATION:
APPLICANT: SHIMOMURA, Takeshi
APPLICANT: KAWAGUCHI, Toshiya
APPLICANT: KITAMURA, Naomi
APPLICANT: MIYAZAWA, Keiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,449
FILING DATE: 22-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,558
FILING DATE: <Unknown>
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: MKN45

SEQUENCE DESCRIPTION: SEQ ID NO: 18
US-09-765-449-18

Query Match 100.0%; Score 206; DB 4; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 60
Db 308 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAAACEKYTSGFDELQRIH 367
Qy 61 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCFRTYGGCYGNKNFEEQQCLESCRG 120
Db 368 FPSDKGHCVLDLPTGLCKESIPRWYNNPFSEHCFRTYGGCYGNKNFEEQQCLESCRG 427
Qy 121 ISKDVFGRLRREIPSTGSEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 180
Db 428 ISKDVFGRLRREIPSTGSEMAVAVFLVICIVVVAAILGYCFFKNQKDFHGHHP 487
Qy 181 PTPASSTVSTTEDTEHLVYNHTTRPL 206
Db 488 PTPASSTVSTTEDTEHLVYNHTTRPL 513

RESULT 4


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US-09-312-283C-182
; Sequence 182, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-182

Query Match      13.1%; Score 27; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.6e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 HHPPTPASSTVSTTDTTEHLVYNHT 203
Db 43 HHPPTPASSTVSTTDTTEHLVYNHT 69

RESULT 5
US-09-188-930-182
; Sequence 182, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 182
; LENGTH: 72
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: {64}...(64)
US-09-188-930-182

Query Match      10.2%; Score 21; DB 3; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 HHPPTPASSTVSTTDTTEHL 197
Db 43 HHPPTPASSTVSTTDTTEHL 63

RESULT 6
US-09-144-20
; Patent No. 5208144
; APPLICANT: SMITH, JOHN A.;RAYCHOWDHURY, RAKTIMA;NILES,JOHN L.
; TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA
; CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR
US-09-312-283C-182
; Sequence 182, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-182

Query Match      13.1%; Score 27; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.6e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 HHPPTPASSTVSTTDTTEHLVYNHT 203
Db 43 HHPPTPASSTVSTTDTTEHLVYNHT 69

RESULT 5
US-09-188-930-182
; Sequence 182, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 182
; LENGTH: 72
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: {64}...(64)
US-09-188-930-182

Query Match      10.2%; Score 21; DB 3; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 HHPPTPASSTVSTTDTTEHL 197
Db 43 HHPPTPASSTVSTTDTTEHL 63

RESULT 6
US-09-144-20
; Patent No. 5208144
; APPLICANT: SMITH, JOHN A.;RAYCHOWDHURY, RAKTIMA;NILES,JOHN L.
; TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA
; CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR

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; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/396,697
; FILING DATE: 22-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 313,682
; FILING DATE: 22-FEB-1989
; APPLICATION NUMBER: 235,211
; FILING DATE: 23-AUG-1988
; SEQ ID NO:20:
; LENGTH: 38
5208144-20

Query Match      5.3%; Score 11; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SGTCQPTQFRC 19
Db 5 SGTCQPTQFRC 15

RESULT 7
5208144-37
; Patent No. 5208144
; APPLICANT: SMITH, JOHN A.;RAYCHOWDHURY, RAKTIMA;NILES,JOHN L.
; TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA
; CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/396,697
; FILING DATE: 22-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 313,682
; FILING DATE: 22-FEB-1989
; APPLICATION NUMBER: 235,211
; FILING DATE: 23-AUG-1988
; SEQ ID NO:37:
; LENGTH: 726
5208144-37

Query Match      5.3%; Score 11; DB 6; Length 726;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SGTCQPTQFRC 19
Db 275 SGTCQPTQFRC 285

RESULT 8
US-09-040-774-2
; Sequence 2, Application US/09040774
; Patent No. 6207811
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kestila, Marjo
; APPLICANT: Lenkkeri, Ulla
; APPLICANT: Mannikko, Minna
; TITLE OF INVENTION: Nephren Gene and Protein
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive, Suite 3200
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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/ CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/040,774
 / FILING DATE: 18 MAR 1998
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Chao, Mark
 / REGISTRATION NUMBER: 37,293
 / REFERENCE/DOCKET NUMBER: 97,842
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (312)913-0001
 / TELEFAX: (312)913-0002
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1241 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 /
 / US-09-040-774-2

Query Match 3.9%; Score 8; DB 3; Length 1241;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 SSTVSTTE 192
 Db 1127 SSTVSTTE 1134

RESULT 9
 US-08-566-800A-32
 ; Sequence 32, Application US/08566800A
 ; Patent No. 5736364
 ; GENERAL INFORMATION:
 ; APPLICANT: Kelley, Robert F.
 ; APPLICANT: Lazarus, Robert A.
 ; APPLICANT: Lee, Geoffrey F.
 ; TITLE OF INVENTION: No. 5736364e1 Factor VIIa Inhibitors
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

/ COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: WinPatIn (Genentech)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/566,800A
 / FILING DATE: 04-Dec-1995
 / CLASSIFICATION: 514
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Kubinec, Jeffrey S.
 / REGISTRATION NUMBER: 36,575
 / REFERENCE/DOCKET NUMBER: P0958B
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 415/225-8228
 / TELEFAX: 415/952-9881
 / TELEX: 910/371-7168
 / INFORMATION FOR SEQ ID NO: 32:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 58 amino acids
 / TYPE: Amino Acid
 / TOPOLOGY: Linear
 /
 / US-08-566-800A-32

Query Match 3.4%; Score 7; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 YGGCYGN 104
 Db 35 YGGCYGN 41

RESULT 10
 US-08-566-800A-37
 ; Sequence 37, Application US/08566800A
 ; Patent No. 5736364
 ; GENERAL INFORMATION:
 ; APPLICANT: Kelley, Robert F.
 ; APPLICANT: Lazarus, Robert A.
 ; APPLICANT: Lee, Geoffrey F.
 ; TITLE OF INVENTION: No. 5736364e1 Factor VIIa Inhibitors
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: WinPatIn (Genentech)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/566,800A
 / FILING DATE: 04-Dec-1995
 / CLASSIFICATION: 514
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Kubinec, Jeffrey S.
 / REGISTRATION NUMBER: 36,575
 / REFERENCE/DOCKET NUMBER: P0958B
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 415/225-8228
 / TELEFAX: 415/952-9881
 / TELEX: 910/371-7168
 / INFORMATION FOR SEQ ID NO: 37:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 58 amino acids
 / TYPE: Amino Acid
 / TOPOLOGY: Linear
 /
 / US-08-566-800A-37

Query Match 3.4%; Score 7; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 YGGCYGN 104
 Db 35 YGGCYGN 41

RESULT 11
 US-08-566-800A-38
 ; Sequence 38, Application US/08566800A
 ; Patent No. 5736364
 ; GENERAL INFORMATION:
 ; APPLICANT: Kelley, Robert F.
 ; APPLICANT: Lazarus, Robert A.
 ; APPLICANT: Lee, Geoffrey F.
 ; TITLE OF INVENTION: No. 5736364e1 Factor VIIa Inhibitors
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 / COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0958B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-566-800A-38

Query Match 3.4%; Score 7; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 YGGCYGN 104
Db 35 YGGCYGN 41

RESULT 12
US-08-566-800A-39
Sequence 39, Application US/08566800A
Patent No. 5736364
GENERAL INFORMATION:
APPLICANT: Kelley, Robert F.
APPLICANT: Lazarus, Robert A.
APPLICANT: Lee, Geoffrey F.
TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0958B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-566-800A-39

Query Match 3.4%; Score 7; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 3.4%; Score 7; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 YGGCYGN 104
Db 35 YGGCYGN 41

RESULT 13
US-08-566-800A-42
Sequence 42, Application US/08566800A
Patent No. 5736364
GENERAL INFORMATION:
APPLICANT: Kelley, Robert F.
APPLICANT: Lazarus, Robert A.
APPLICANT: Lee, Geoffrey F.
TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0958B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-566-800A-42

Query Match 3.4%; Score 7; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 YGGCYGN 104
Db 35 YGGCYGN 41

RESULT 14
US-08-566-800A-44
Sequence 44, Application US/08566800A
Patent No. 5736364
GENERAL INFORMATION:
APPLICANT: Kelley, Robert F.
APPLICANT: Lazarus, Robert A.
APPLICANT: Lee, Geoffrey F.
TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0958B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-566-800A-44

Query Match 3.4%; Score 7; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 YGGCYGN 104
Db 35 YGGCYGN 41

RESULT 15
US-08-566-800A-45
Sequence 45, Application US/08566800A
Patent No. 5736364
GENERAL INFORMATION:
APPLICANT: Kelley, Robert F.
APPLICANT: Lazarus, Robert A.
APPLICANT: Lee, Geoffrey F.
TITLE OF INVENTION: No. 5736364e1 Factor VIIa Inhibitors
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0958B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids

TYPE: Amino Acid
TOPOLOGY: Linear
US-08-566-800A-45
Query Match 3.4%; Score 7; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 YGGCYGN 104
Db 35 YGGCYGN 41

Search completed: April 22, 2004, 10:26:18
Job time : 24 secs